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(54) Title: YEAST TELOMERASE COMPONENTS AND METHODS USING THEM		
(57) Abstract Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of <i>S. cerevisiae</i> telomerase and various telomerase-associated polypeptides. <div style="text-align: right; margin-top: 200px;">196 158 <hr/>249</div>		

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DESCRIPTIONTELOMERASE COMPOSITIONS AND METHODS5 BACKGROUND OF THE INVENTION

The present invention is a continuation-in-part of co-pending U.S. Patent Application Serial No. 08/326,781, filed October 20, 1994, the entire text and figures of which disclosure is specifically incorporated herein by
10 reference without disclaimer. The U.S. Government owns rights in the present invention pursuant to National Institutes of Health Grants GM43893 and CA14599.

15 A. Field of the Invention

The present invention relates to telomerase compositions and methods connected therewith. Particularly disclosed are genes encoding the template
20 RNA of telomerase in *Saccharomyces cerevisiae* and various telomerase-associated proteins. Methods of using such genes and other related biological components are also provided.

25 B. Description of the Related Art

DNA polymerases synthesize DNA in a 5' to 3' direction and require a primer to initiate synthesis. These restrictions pose a problem for the complete
30 replication of linear chromosomes (Watson, 1972; Olovnikov, 1973). In the absence of a specialized mechanism to maintain terminal sequences, multiple replication cycles would cause chromosomes to progressively shorten from their ends.

35

Telomeres are specialized nucleoprotein complexes that constitute the ends of eukaryotic chromosomes and

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protect them from degradation and end-to-end fusion
(Zakian, 1989; Blackburn, 1991; Price, 1991; Henderson &
Larson, 1991; Wright et al., 1992; Blackburn, 1994).
When telomeres are absent, the instability of non-
5 telomeric chromosomal ends leads to chromosome loss
(Sandell & Zakian, 1993). In addition, telomeres are
required for the complete replication of chromosomes
(Zakian, 1989; Blackburn, 1991; Price, 1991; Henderson &
Larson, 1991; Wright et al., 1992; Blackburn, 1993;
10 1994).

In many eukaryotes, telomeres are composed of simple
tandem repeats, with the 3'-terminal strand composed of
G-rich sequences (Zakian, 1989; Blackburn, 1991; Price,
15 1991; Henderson & Larson, 1991; Wright et al., 1992;
Blackburn, 1994). Certain insights into the mechanism by
which telomeric DNA is maintained has come from the
identification of telomerase activity in several species
of ciliates, as well as in extracts of *Xenopus*, mouse,
20 and human cells (Greider & Blackburn, 1985; 1987; 1989;
Zahler & Prescott, 1988; Morin, 1989; Prowse et al.,
1993; Shippen-Lentz & Blackburn, 1989; Mantell & Greider,
1994).

25 Telomerase is a ribonucleoprotein enzyme that
elongates the G-rich strand of chromosomal termini by
adding telomeric repeats (Blackburn, 1993). This
elongation occurs by reverse transcription of a part of
the telomerase RNA component, which contains a sequence
30 complementary to the telomere repeat. Following
telomerase-catalyzed extension of the G-rich strand, the
complementary DNA strand of the telomere is presumably
replicated by more conventional means.

35 Germline cells, whose chromosomal ends must be
maintained through repeated rounds of DNA replication, do
not decrease their telomere length with time, presumably

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due to the activity of telomerase (Allsopp et al., 1992). In contrast, somatic cells appear to lack telomerase, and their telomeres shorten with multiple cell divisions (Allsopp et al., 1992; Harley et al., 1990; Hastie
5 et al., 1990; Lindsey et al., 1991; Vaziri et al., 1993; Counter et al., 1992; Shay et al., 1993; Klingelhutz et al., 1994; Counter et al., 1994a;b).

Telomerase is believed to have a role in the process
10 of cell senescence (de Lange, 1994; Greider, 1994; Harley et al., 1992). The repression of telomerase activity in somatic cells is likely to be important in controlling the number of times they divide. Indeed, the length of telomeres in primary fibroblasts correlates well with the
15 number of divisions these cells can undergo before they senescence (Allsopp et al., 1992). The loss of telomeric DNA may signal to the cell the end of its replicative potential, as part of an overall mechanism by which multicellular organisms limit the proliferation of their
20 cells.

Due to its role in controlling replication, telomerase has also recently been implicated in oncogenesis (de Lange, 1994; Greider, 1994; Harley
25 et al., 1992). It is thought that late stage tumors probably require the reactivation of telomerase in order to avoid total loss of their telomeres and massive destabilization of their chromosomes. Immortalized cell lines produced from virally transformed cultures have
30 active telomerase and stable telomere lengths (Counter et al., 1992; Shay et al., 1993; Klingelhutz et al., 1994; Counter et al., 1994b). Recently, telomerase activity has also been detected in human ovarian carcinoma cells (Counter et al., 1994a).

35

Telomerase is thus an important component of eukaryotic cells, the dysfunction of which can have

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significant consequences. Although present knowledge concerning telomerase is increasing, there is a marked need for individual telomerase components to be isolated and for further analytical methods to be developed. The
5 creation of a system for manipulating telomerase in a genetically tractable eukaryotic organism would be particularly valuable.

SUMMARY OF THE INVENTION

10

The present invention overcomes these and other drawbacks inherent in the prior art by providing purified telomerase components and systems for isolating further components and for developing agents with the capacity to
15 modify telomerase actions. Particular aspects of this invention concern the isolation and uses of several telomerase-associated genes from *Saccharomyces cerevisiae*, including the telomerase RNA template gene.

20

In certain aspects, this invention concerns nucleic acid segments that hybridize to, or that have sequences in accordance with, SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23. SEQ ID NO:1 represents a telomerase RNA template-encoding
25 sequence, also termed *TLCl*; and each of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 and SEQ ID NO:23 represent sequences that encode telomerase-associated polypeptides, also termed *STR* sequences (*STR1*, *STR3*, *STR4*, *STR5* and *STR6*, respectively).

30

Both the gene *TLCl* (SEQ ID NO:1 and the complementary sequence, SEQ ID NO:4), and the template RNA, include a CA-rich region. The CA-rich region is represented by SEQ ID NO:3. In the RNA template, the CA-
35 rich region is reversed transcribed to synthesize the GT-rich telomeric repeats. An example of the GT-rich telomeric sequence is represented by SEQ ID NO:2.

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The present invention generally concerns non-ciliate eukaryotic telomerase components. These are represented by telomerase components from mammalian cells, including human cells, and telomerase components from other non-ciliate species. One significant contribution of this invention is the development of methods of utilizing telomerase components, which methods are functional in useful eukaryotic cells. "Useful eukaryotic cells" particularly include human cells, as these are directly relevant to the development of diagnostics and therapeutics for human use, and cells of genetically tractable eukaryotic organisms, as these are recognized to have significant value in scientific terms and, ultimately, in drug development. The preferred non-ciliate telomerase components of the invention are thus mammalian, drosophila and yeast telomerase components.

A. DNA Segments and Vectors

The invention thus provides nucleic acid segments that are characterized as nucleic acid segments that include a sequence region that consists of at least 17 contiguous nucleotides that have the same sequence as, or are complementary to, 17 contiguous nucleotides of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23.

The nucleic acid segments of the invention are further characterized as being of from 17 to about 10,000 nucleotides in length, which nucleic acid segments hybridize to the nucleic acid segment of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or the complement thereof, under standard hybridization conditions.

35

"Complementary" or "complement", in terms of nucleic acid segments that are complementary to those listed

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above, or that hybridize to a complement of such nucleic acid segments, means that the nucleic acid sequences are capable of base-pairing to a given sequence, such as the sequences of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, according to the standard Watson-Crick complementarity rules. That is, the larger purines will base pair with the smaller pyrimidines to form combinations of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T), in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA.

Encompassed within the nucleic acid sequences of the invention are full-length DNA sequences or other DNA segments that have a sequence region that encodes a peptide, polypeptide or protein and that may be used, for example, in recombinant expression. Also included within the nucleic acid sequences are DNA and RNA segments for use in nucleic acid hybridization embodiments, such as in cloning.

The smaller nucleic acid segments may be termed probes and primers. The individual sequences of 17, 20, 30, 50 or so nucleotide sequence stretches, for example, may be readily identified by "breaking down" the longer sequences disclosed herein to provide one or more shorter sequences. Using an exemplary length of 17 bases, each of the 17-mer possibilities from the DNA sequences described herein have been defined and are listed in Table 2.

In certain embodiments, the invention provides isolated DNA segments and recombinant vectors that have one or more sequence regions that encode one or more non-ciliate eukaryotic telomerase components, and preferably, those that encode one or more yeast (*S. cerevisiae*) telomerase components. The creation and use of

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recombinant host cells, through the application of DNA technology, that express yeast or other non-ciliate eukaryotic telomerase components is also encompassed by the invention.

5

As used herein, the term "telomerase component" refers to a biological component that is associated with a non-ciliate eukaryotic telomerase complex, such as a mammalian, drosophila or yeast telomerase component.

10 Preferably, the telomerase components will be associated with a yeast telomerase complex. A "telomerase complex" in this sense is a ribonucleoprotein enzyme complex that functions to elongate the G-rich strand of eukaryotic, and preferably yeast, chromosomal termini by adding
15 telomeric repeats. Telomerase components (or telomerase-associated components) therefore include both RNA and polypeptidyl components.

An important component of telomerase is the
20 telomerase RNA template or template sequence. The term "telomerase RNA template", as used herein, refers to a non-ciliate eukaryotic, such as a mammalian, drosophila, or preferably, a yeast telomerase RNA component that includes a sequence that is complementary to the telomere
25 repeat, i.e., that is complementary to the G-rich or GT-rich sequences of chromosomal termini. The telomerase RNA template is thus an isolated RNA component that has a C-rich or CA-rich sequence and that, by interacting with other telomerase components, functions to extend
30 telomeric repeats. The telomerase RNA template may also be defined as the telomerase substrate for reverse transcription.

Further telomerase components are telomerase-
35 associated proteins and polypeptides. The "telomerase-associated proteins and polypeptides" of this invention are proteins, polypeptides or peptides that are required

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for telomerase function in non-ciliate eukaryotic cells, and preferably, in yeast cells. Such telomerase-associated proteins and polypeptides will generally be physically and functionally associated with the telomerase complex in the nucleus, however, they may also be proteins or polypeptides that only associate with the telomerase complex for certain periods of time, at defined points of the cell cycle, or may be present only in certain cell types of a multicellular organism.

10

Telomerase-associated proteins, polypeptides and peptides may have either functional or structural roles within the telomerase complex. That is, they may have a catalytic or regulatory role, or may form the scaffolding of the telomerase structure. The telomerase-associated proteins or polypeptides may function only in terms of telomerase activity, i.e., they may be telomerase-restricted; or they may have other biological functions within the cell nucleus, such as in other aspects of chromosome replication and stability, or may even have cytoplasmic functions.

The telomerase DNA segments of the present invention are thus DNA segments isolatable from non-ciliate eukaryotic cells, and preferably, from yeast cells, that are free from total genomic DNA and that include a sequence region that is capable of expressing a telomerase RNA or polypeptide component. The DNA segments may, in certain embodiments, also be defined as those capable of inhibiting the telomerase activity of a cell by over-expression in a cell that previously contained telomerase activity. In further embodiments, the DNA segments may be defined as those capable of conferring telomerase activity to a host cell when incorporated into a cell that has been rendered deficient in such activity.

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As used herein, the term "DNA segment" refers to a DNA molecule that has been isolated free of total genomic DNA of a particular species, such as a mammal, drosophila or yeast species. Therefore, a DNA segment that
5 comprises a sequence region that encodes a telomerase-associated component refers to a DNA segment that includes telomerase-associated component coding sequences or regions, yet is isolated away from, or purified free from, total genomic DNA of the species from which the DNA
10 segment is obtained. Included within the term "DNA segment", are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like.

15 Similarly, a telomerase-associated gene is a DNA segment comprising an isolated or purified gene that includes a sequence region that encodes a component associated with a mammalian, drosophila, or preferably, with a yeast telomerase. The term "an isolated gene
20 associated with a non-ciliate eukaryotic telomerase", as used herein, refers to a DNA segment including telomerase RNA or protein coding sequences or regions and, in certain aspects, regulatory sequences, isolated substantially away from other naturally occurring genes
25 or encoding sequences. In this respect, the term "gene" is used for simplicity to refer to a functional RNA, protein, polypeptide or peptide encoding unit or region. As will be understood by those in the art, this functional term includes both genomic sequences, cDNA
30 sequences and smaller engineered gene segments that express, or may be adapted to express, RNA molecules, proteins, polypeptides or peptides.

"Isolated substantially away from other coding
35 sequences" means that the gene of interest, in this case a telomerase-associated gene, forms the significant part of the sequence or coding region of the DNA segment, and

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that the DNA segment does not contain large portions of naturally-occurring coding DNA, such as large chromosomal fragments or other functional genes or cDNA coding regions. Of course, this refers to the DNA segment as
5 originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

In particular embodiments, the invention concerns isolated DNA segments and recombinant vectors
10 incorporating DNA sequences that include an isolated gene or sequence region that encodes a non-ciliate eukaryotic telomerase RNA template, such as a mammalian, drosophila, or preferably, a yeast telomerase RNA template. This aspect of the invention is exemplified by DNA segments
15 and genes that encode the *S. cerevisiae* telomerase RNA template sequence of CACCACACCCACACAC (SEQ ID NO:3).

A variety of oligonucleotides, DNA segments and genes that encode the CACCACACCCACACAC (SEQ ID NO:3)
20 telomerase RNA template sequence are made possible by the discovery of the present inventors'. These include sequences from SEQ ID NO:1, and the complementary strand, SEQ ID NO:4. The sequence from SEQ ID NO:1 that includes the template-encoding region of CACCACACCCACACAC (SEQ ID
25 NO:3) is particularly represented by the contiguous DNA sequence from position 468 to position 483 of SEQ ID NO:1. Such DNA segments will have a minimum length of 17 nucleotides, and are exemplified by the contiguous DNA sequences from position 467 to position 483, or from
30 position 468 to position 484, of SEQ ID NO:1.

DNA segments longer than 17 bases are also contemplated, in increments of single integers up to and including the 1301 bases of SEQ ID NO:1, and even longer.
35 The contiguous sequences from SEQ ID NO:1 may be equidistant around the template-encoding region of SEQ ID NO:3, or they may have the SEQ ID NO:3 region located

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substantially towards the beginning or towards the end of the given sequence. DNA segments may thus have sequences in accordance with the contiguous sequences between about position 450 or 460 and about position 485 of SEQ ID NO:1; between about position 300 or 400 and about position 500, 600 or 700 of SEQ ID NO:1; between about position 100 or 200 and about position 800, 900, 1000, 1100 or 1200 of SEQ ID NO:1; or between any of the aforementioned ranges and intermediates thereof. DNA segments and isolated genes that include the full-length DNA sequence of SEQ ID NO:1 are also contemplated.

In further embodiments, the invention provides isolated DNA segments, genes and vectors incorporating DNA sequences that encode a non-ciliate eukaryotic telomerase-associated polypeptide, such as a mammalian, drosophila or yeast, telomerase-associated polypeptide, as exemplified by yeast polypeptides that includes within their amino acid sequence a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

The term "a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24" means that a contiguous sequence is present that substantially corresponds to a contiguous portion of one of the afore-mentioned sequences and has relatively few amino acids that are not identical to, or a biologically functional equivalent of, the amino acids of SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24. The term "biologically functional equivalent" is well understood in the art and is further defined in detail herein. Accordingly, sequences that have between about 70% and about 80%; or more preferably, between about 81% and about 90%; or even more preferably, between about 91% and about 99%; of amino acids that are identical or functionally equivalent to the amino acids

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of SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24 will be sequences in accordance with the present invention.

5 The protein-encoding DNA segments, genes and vectors may include within their sequence region a contiguous nucleic acid sequence from SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23. The term "a
10 contiguous nucleic acid sequence from SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23" is used in the same sense as described above and means that the nucleic acid sequence substantially corresponds to a contiguous portion of one of the designated sequences and has relatively few codons that are not identical, or
15 functionally equivalent, to the codons of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23. The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers
20 to codons that encode biologically equivalent amino acids, as is known in the art and further described herein (see Table 1).

 Protein-encoding DNA segments and genes of the
25 present invention may encode a full length telomerase-associated protein or polypeptide, as may be used in expressing the protein. Such DNA segments are exemplified by those that comprise an isolated gene that includes a contiguous DNA sequence substantially as shown
30 between position 54 and position 1799 of SEQ ID NO:29, that encodes a polypeptide substantially as shown in SEQ ID NO:16; or that includes a contiguous DNA sequence substantially as shown between position 78 and position 1094 of SEQ ID NO:30, that encodes a polypeptide
35 substantially as shown in SEQ ID NO:18; or that includes a contiguous DNA sequence substantially as shown between position 2 and position 2368 of SEQ ID NO:19, that

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encodes a polypeptide substantially as shown in SEQ ID NO:20; or that includes a contiguous DNA sequence substantially as shown between position 55 and position 699 of SEQ ID NO:31, that encodes a polypeptide
5 substantially as shown in SEQ ID NO:22; or that includes a contiguous DNA sequence substantially as shown between position 3 and position 1955 of SEQ ID NO:23, that encodes a polypeptide substantially as shown in SEQ ID NO:24.

10

For both protein expression and hybridization, the nucleic acid segments used may include the full length versions of any of the telomerase-associated genes disclosed herein, or their biological equivalents,
15 including their complementary sequences where hybridization is concerned. This is exemplified by DNA segments that have, or that comprise a sequence region that has, the 1301 nucleotides of SEQ ID NO:1, the 1882 nucleotides of SEQ ID NO:29, the 1094 nucleotides of SEQ
20 ID NO:30, the 2434 nucleotides of SEQ ID NO:19, the 807 nucleotides of SEQ ID NO:31, the 2117 nucleotides of SEQ ID NO:23, or any substantially equivalent sequences.

Further, the present DNA segments may be used to
25 express protein fragments or peptides, for example, peptides of from about 15 to about 30, about 50 or about 100 amino acids in length. The peptides may, of course, be of any length between or around such stated ranges, with "about" meaning a range of lengths in positive
30 integers between each above-listed reference point and higher, with 12-15 or so being the minimum length. Appropriate coding sequences and regions may be readily identified from any of the regions of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23.

35

The sequence or coding regions of the invention will be a minimum length of 17 nucleotides, and will most

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often be longer than this, such as upwards of about 40-50 nucleotides in length or so. The maximum length of the DNA segments is not limited by the length of the coding regions themselves, so that DNA segments of about 1,000,
5 about 3,000, about 5,000 and 10,000 or even longer are contemplated. It will be readily understood that all lengths intermediate between the above-quoted ranges are also included.

10 It will also be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids or 5' or 3' sequences, and yet still be substantially as shown in one of the sequences disclosed herein, so long as the
15 sequence meets the criteria set forth above. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either of the 5' or 3' portions of the coding region or may include various
20 internal sequences, i.e., introns, which are known to occur within genes.

Excepting intronic or flanking regions, and allowing for the degeneracy of the genetic code, sequences that
25 have between about 70% and about 80%; or more preferably, between about 80% and about 90%; or even more preferably, between about 90% and about 99% of nucleotides that are identical to the nucleotides of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID
30 NO:23 will be sequences that are substantially as shown in such sequences. From the inventors' experience, sequences with 70% identity or higher are expected to be telomerase-related sequences.

35 The nucleic acid segments of the present invention, regardless of the length of any coding sequences themselves, may be combined with other nucleic acid

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sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is
5 therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol.

10 As stated above, the invention is not limited to the particular sequences of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23 (nucleic acid), or SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24 (amino acid). In
15 terms of expression, recombinant vectors may therefore variously include the telomerase-associated protein coding regions themselves, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides that
20 nevertheless include such telomerase-associated protein coding regions or may encode biologically functional equivalent proteins or peptides that have variant amino acids sequences.

25 For protein expression embodiments, the DNA segments may include biologically functional equivalent protein-coding sequences that have arisen as a consequence of codon redundancy and functional equivalency, as is known to occur naturally within biological sequences.
30 Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being
35 exchanged. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques, e.g., to introduce improvements to the

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antigenicity of the protein or to test telomerase mutants in order to examine their activity at the molecular level.

5 If desired, one may also prepare fusion proteins and peptides, e.g., where the telomerase-associated protein coding regions are aligned within the same expression unit with other proteins or peptides having desired functions, such as for purification or immunodetection
10 purposes (e.g., proteins that may be purified by affinity chromatography and enzyme label coding regions, respectively).

Recombinant vectors form further aspects of the
15 present invention. Particularly useful vectors are contemplated to be those vectors in which an RNA or protein coding portion of a DNA segment, whether encoding an RNA template, a full length protein or smaller peptide, is positioned under the control of a promoter.
20 The promoter may be in the form of the promoter that is naturally linked to a telomerase-associated gene, as may be obtained by isolating the 5' non-coding sequences located upstream of the coding segment or exon, for example, using recombinant cloning and/or PCR technology,
25 in connection with the compositions disclosed herein.

In other expression embodiments, it is contemplated that certain advantages will be gained by positioning a coding DNA segment or sequence region under the control
30 of a recombinant, or heterologous, promoter. As used herein, a recombinant or heterologous promoter is intended to refer to a promoter that is not normally associated with a telomerase-associated gene in its natural environment. Such promoters may include yeast
35 promoters normally associated with other genes, and/or promoters isolated from any other bacterial, viral, insect or mammalian cell.

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Naturally, it will be important to employ a promoter that effectively directs the expression of the DNA segment in the cell type, organism, or even animal, chosen for expression. The use of promoter and cell type combinations for protein expression is generally known to those of skill in the art of molecular biology, for example, see Sambrook et al. (1989). The promoters employed may be constitutive, or inducible, and can be used under the appropriate conditions to direct high level expression of the introduced DNA segment, such as is advantageous in the large-scale production of recombinant proteins or peptides.

Preferred promoter systems contemplated for use in high-level expression in *S. cerevisiae* include, but are not limited to, the GAL1, MET3, and PGK promoter systems. For conditional alleles, as may be used in cellular studies of the RNA template, a chimeric fusion of an RNA template gene may be placed under the regulation of a heterologous promoter. Appropriate promoters include the MET3 promoter, which is repressed in the presence of methionine and induced when methionine is absent from the medium; and the GAL1,10 UAS, as described in Example XI.

B. Nucleic Acid Hybridization

In addition to their use in directing the expression of telomerase-associated RNA and protein components, the nucleic acid sequences disclosed herein also have a variety of other uses, for example, in nucleic acid hybridization embodiments. The ability of nucleic acid probes or primers to specifically hybridize to the telomerase-associated nucleic acid sequences disclosed herein will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are envisioned, including the use of the sequence information for the preparation of mutant

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species primers, or primers for use in preparing other genetic constructs.

5 The present invention thus concerns nucleic acid segments of 17 nucleotides in length, or longer, that hybridize to the telomerase-associated sequences of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or their complements, under standard hybridization conditions. This provides another physical and functional definition for identifying additional sequences in accordance with the invention, as well as defining useful sub-sequences, such as primers.

15 The nucleic acids that hybridize to the sequences of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, may be 17 nucleotides in length or longer, such as about 20, about 25, about 30, about 50, about 75, about 100, about 150, about 200, about 250, about 500, about 750 or about 1,000 nucleotides in length, or even longer. As the length of the nucleic acid segment that hybridizes is not solely a function of the length of the substantially complementary sequence region, these nucleic acid segments may also be about 2,000, about 3,000, about 5,000 or about 10,000 nucleotides in length or longer, so long as the total length does not prevent hybridization under the conditions defined herein.

30 As with the sequence or coding regions defined hereinabove, it will be readily understood that any intermediate length between the quoted ranges is included, such as 17, 18, 19, 20, 21, 22, 23, etc; 50, 51, 52, 53, etc.; 100, 101, 102, 103, etc.; including all positive integers through the 150-500; 500-1,000; 1,000-2,000; 2,000-5,000; and 5,000-10,000 ranges, up to and including sequences of about 12,001, 12,002, 13,001, 13,002 and the like.

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The total size of nucleic acid segment or fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. The use of a
5 hybridization probe of about 17 nucleotides in length allows the formation of a duplex molecule that is both stable and selective.

Accordingly, the nucleotide sequences of the
10 invention may be used for their ability to selectively form duplex molecules with complementary stretches of telomerase-associated genes or cDNAs. Depending on the application envisioned, one will desire to employ varying conditions of hybridization to achieve varying degrees of
15 selectivity of probe towards target sequence.

For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, e.g., one will select
20 relatively low salt and/or high temperature conditions that tolerate little, if any, mismatch between the probe and the template or target strand. Standard high stringency hybridization conditions are described in the hybridization protocols set forth herein in the detailed
25 description.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, or where one
30 seeks to isolate telomerase-associated sequences from related species, functional equivalents, or the like, less stringent hybridization conditions are useful to allow formation of the heteroduplex. In these circumstances, one may desire to employ standard low
35 stringency hybridization conditions, which are also described in the hybridization protocols set forth in the detailed description.

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Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more
5 stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex, in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on
10 the desired results.

Where hybridization probes or primers are to be designed from a consideration of the longer sequences disclosed herein, they may be selected from any portion
15 of any of the nucleic acid sequences. All that is required is to review the sequences and to select any continuous portion of the sequence, from 17 nucleotides in length up to and including the full length sequence.

20 Once the coding sequence of a telomerase-associated gene has been determined, various primers can be designed around that sequence. Primers may be of any length, but typically, are 17, 20, 25 or 30 bases or so in length. By assigning numeric values to a sequence, for example,
25 the first residue is 1, the second residue is 2, and the like, an algorithm defining all primers is:

$$n \text{ to } n + y$$

30 where n is an integer from 1 to the last number of the sequence and y is the length of the primer minus one, in the above cases (16, 19, 24, 29), where $n + y$ does not exceed the last number of the sequence. For example, for the *TLC1* gene, n is 1 to 1301. Thus, for a 17-mer, the
35 probes correspond to bases 1 to 17, 2 to 18, 3 to 19.... up to 1285 to 1301. Table 2 herein sets forth the number of contiguous 17-mer sequences that may be obtained from

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the sequences of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or their complements.

5 The choice of probe and primer sequences may be governed by various factors, such as, by way of example only, one may wish to employ primers from towards the termini of the total sequence, or from the ends of any functional domain-encoding sequences, in order to amplify
10 further DNA; one may employ probes corresponding to the entire DNA, or to the RNA template region, to clone template genes from other species or to clone further telomerase template-like or homologous genes from any species including human; one may also design appropriate
15 probes or primers to screen biological samples to identify cells with inappropriate telomerase levels or activity, as may be related to cancer or even to infertility.

20 The process of selecting and preparing a nucleic acid segment that includes a contiguous sequence from within SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23 may be readily achieved by, for example, directly synthesizing the
25 fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR technology of U.S. Patent 4,683,202 and U.S. Patent 4,682,195 (each
30 incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology. Of course, smaller nucleic acid
35 fragments may also be obtained by other techniques such as, e.g., by mechanical shearing or by restriction enzyme digestion.

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In certain embodiments, it will often be advantageous to employ nucleic acid sequences of the present invention in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In certain embodiments, one will likely desire to employ a fluorescent label or an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known that can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary nucleic acid-containing samples.

In general, it is envisioned that the hybridization probes described herein will be useful both as reagents in solution hybridization as well as in embodiments employing a solid phase. In embodiments involving a solid phase, the test DNA (or RNA) is adsorbed or otherwise affixed to a selected matrix or surface. This fixed, single-stranded nucleic acid is then subjected to specific hybridization with selected probes under desired conditions. The selected conditions will depend on the particular circumstances based on the particular criteria required (depending, for example, on the G+C contents, type of target nucleic acid, source of nucleic acid, size of hybridization probe, etc.). Following washing of the hybridized surface so as to remove nonspecifically bound probe molecules, specific hybridization is detected, or even quantified, by means of the label.

35

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C. Further Telomerase Compositions

The present invention further includes isolated RNA segments, of from 17 to about 1,500 nucleotides in length, that comprise a non-ciliate, or preferably, a yeast telomerase RNA template. The isolated RNA segments will be obtained free from total nucleic acids, chromosomes and intact telomerase complexes, and will include a non-ciliate eukaryotic, or preferably, a yeast telomerase RNA template. This is exemplified by RNA segments including the *S. cerevisiae* RNA template sequence of CACCACACCCACACAC (SEQ ID NO:3).

Isolated RNA segments that include the minimum functional mammalian, drosophila or yeast telomerase RNA template coding sequences and the minimum upstream sequences necessary for expression are also contemplated. These may be identified as described herein in Example XI and will be useful in mutant analysis, promoter and expression analysis and creation of conditional mutants.

Isolated RNA segments that have substantially the same secondary structure as the RNA segment encoded by the sequence of SEQ ID NO:1 are also included within the scope of the present invention. This may be assessed by techniques, and computer programs, that predict secondary structure based on the primary sequence of the RNA. The secondary structure predictions are supported by mutant/function analysis, as is well known in the art. That is, given the predicted structure, it is straightforward for the ordinary artisan to accurately predict the effects of certain sets of mutations in the RNA.

Further compositions in accordance with this invention include affinity columns that comprise a deoxyoligonucleotide attached to a solid support, where

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the deoxyoligonucleotide includes a sequence complementary to a non-ciliate, or preferably, a yeast telomerase RNA template sequence. Such deoxyoligonucleotides and affinity columns will be
5 capable of binding eukaryotic, or preferably, yeast telomerase complexes, enabling their purification. As the template RNA includes the CA-rich template region, an appropriate column-bound bait will be a GT-rich DNA sequence, as represented, by way of example only, by SEQ
10 ID NO:2.

The oligonucleotides may be attached to any one of a variety of solid supports for use in standard column chromatography or in FPLC or HPLC techniques.
15 Oligonucleotides may be attached using a variety of appropriate methods, such as, by way of example, using direct chemical conjugation, or other means such as biotin-avidin linkers, and the like. All such techniques are routine in the art.

20 Still further embodiments of the present invention concern recombinant host cells that contain or incorporate a DNA segment or recombinant vector that comprises an isolated gene associated with non-ciliate
25 eukaryotic, or preferably, with yeast telomerase. The telomerase-associated components, whether they be cDNA or genomic, may be used in expression systems for the recombinant preparation of RNA templates or telomerase-associated polypeptides.

30 As used herein, the term "engineered" or "recombinant" cell is intended to refer to a cell into which an exogenous DNA segment or gene, such as a cDNA or gene encoding a telomerase-associated component has been
35 introduced. Therefore, engineered cells are distinguishable from naturally occurring cells that do not contain a recombinantly introduced exogenous DNA

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segment or gene. Engineered cells are thus cells having a gene or genes introduced through the hand of man. Recombinantly introduced genes will either be in the form of a cDNA gene (i.e., they will not contain introns), a
5 copy of a genomic gene, or will include genes positioned adjacent to a promoter not naturally associated with the particular introduced gene.

10 The engineering of DNA segment(s) for expression in prokaryotic or eukaryotic systems is performed using techniques known to those of skill in the art, and further described herein in detail. It is believed that virtually any prokaryotic or eukaryotic host cell system may be employed in the expression of one or more
15 telomerase-associated components, with yeast systems being preferred in certain embodiments. Telomerase-associated polypeptides may also be as fusions with, e.g., β -galactosidase, ubiquitin, *Schistosoma japonicum* glutathione S-transferase, and the like.

20 To achieve expression, one would position the telomerase coding sequences adjacent to and under the control of a promoter. It is understood in the art that to bring a coding sequence under the control of such a
25 promoter, one positions the 5' end of the transcription initiation site of the transcriptional reading frame of the protein between about 1 and about 50 nucleotides or so "downstream" of (i.e., 3' of) the chosen promoter.

30 Where eukaryotic expression is contemplated, one will also typically desire to incorporate into the transcriptional unit which includes the enzyme, an appropriate polyadenylation site (e.g., 5'-AATAAA-3') if one was not contained within the original cloned segment.
35 Typically, the poly A addition site is placed about 30 to 2000 nucleotides "downstream" of the termination site of

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the protein at a position prior to transcription termination.

Generally speaking, it may be more convenient to
5 employ as the recombinant gene a cDNA version of the
gene. It is believed that the use of a cDNA version will
provide advantages in that the size of the gene will
generally be much smaller and more readily employed to
transfect the targeted cell than will a genomic gene,
10 which will typically be up to an order of magnitude
larger than the cDNA gene. However, the inventors do not
exclude the possibility of employing a genomic version of
a particular gene where desired.

15 The recombinant host cells of the invention will
effectively expresses a DNA segment to produce a
telomerase RNA template or a polypeptide associated with
telomerase. The invention thus further includes
recombinant gene products that are prepared by expressing
20 a eukaryotic, or preferably, a yeast telomerase-
associated gene in a recombinant host cell and purifying
the expressed gene product away from total recombinant
host cell components. The gene products include
telomerase RNA templates, proteins, polypeptides and
25 peptides associated with telomerase, and combinations and
equivalents thereof.

The preparation of such recombinant gene products is
preferably achieved by using a DNA segment of the
30 invention in the preparation of a recombinant vector in
which a telomerase-associated gene is positioned under
the control of a promoter. The recombinant vector is
then introduced into a recombinant host cell, which is
cultured under conditions effective, and for a period of
35 time sufficient, to allow expression of the telomerase-
associated gene, which thus allows the expressed gene
product to be collected, giving a purified preparation.

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The invention further concerns recombinant RNA segments that include non-ciliate telomerase RNA templates, such as mammalian, drosophila, or preferably, yeast telomerase RNA templates; and recombinant protein and polypeptide compositions, free from total cell components, that comprise one or more purified non-ciliate, or preferably, yeast telomerase-associated components. These are exemplified by polypeptides that include a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

The terms "purified telomerase-associated polypeptide and RNA template", as used herein, refer to telomerase-associated polypeptide or RNA template compositions, isolatable from eukaryotic, or preferably, from yeast cells, wherein the polypeptide or RNA is purified to any degree relative to its naturally-obtainable state, e.g., relative to its purity within a cellular extract. More preferably, "purified" refers to telomerase-associated polypeptide or RNA template compositions that have been subjected to fractionation to remove various non-telomerase components. "Substantially purified" native and recombinant telomerase RNA templates and polypeptides are also preparable using the methods of the invention.

To prepare a purified telomerase-associated component in accordance with the present invention one would subject a composition to fractionation to remove various non-telomerase-associated components. Various techniques suitable for use in RNA and protein purification will be well known to those of skill in the art. Protein purification techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies, and the like, or by heat denaturation, followed by centrifugation; chromatography steps such as

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ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of such and other techniques.

5

Specific examples of purification schemes for use in the present invention are those including initial separation of nuclear proteins, followed by gradient centrifugation methods (equilibrium and sedimentation velocity), column chromatography and gel electrophoresis, as described in Example XV. Specific binding to RNA or DNA segments related to the telomerase template sequences, including affinity column binding embodiments, is also envisioned to be particularly useful.

15

For assays of intact or relatively intact telomerase complexes, deoxyoligonucleotide substrates, representing 3' G-rich telomere tails, are incubated in cellular extracts containing telomerase with ³²P-labeled dNTP's (typically dGTP or dTTP). The products of telomerase elongation on the input deoxyoligonucleotide substrate may then be detected by, e.g., gel electrophoresis and autoradiography. A series of substrates is also preferably used, as described in Example XV.

25

Although preferred for use in certain embodiments, there is no general requirement that the RNA or proteins always be provided in their most purified state. Indeed, it is contemplated that less substantially purified telomerase-associated components, which are nonetheless enriched relative to their natural state, will have utility in certain embodiments. These include, for example, certain binding assays, screening protocols, titration of components, and the like. Inactive protein fractions also have utility, for example, in antibody generation.

35

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In further embodiments, the invention also provides polyclonal or monoclonal antibodies that bind to a non-ciliate, and preferably, to a yeast telomerase-associated polypeptide, as exemplified by an antibody that has
5 binding affinity for a protein or peptide that includes a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24. Cross-reactive antibodies are also encompassed by the invention, as may be identified by employing a
10 competition binding assay, such as an ELISA or RIA, as are well known in the art.

Particular techniques for preparing antibodies in accordance with the invention are disclosed herein, which
15 methods generally comprise administering to an animal a composition comprising an immunologically effective amount of a telomerase-associated component protein, peptide or other epitopic composition. By "immunologically effective amount" is meant an amount of
20 a telomerase-associated protein or peptide composition that is capable of generating an immune response in the recipient animal, and particularly, in this case, generating an antibody or B cell response.

Any of the DNA, RNA, proteins, polypeptides and antibodies of this invention may also be linked to a detectable label, such as a radioactive, fluorogenic, biological, chromogenic or even a nuclear magnetic spin
25 resonance label. Biolabels such as biotin and enzymes that are capable of generating a colored product upon
30 contact with a chromogenic substrate will be preferred in certain embodiments. Exemplary enzyme labels include alkaline phosphatase, hydrogen peroxidase, urease and glucose oxidase enzymes.

35

In still further embodiments, the invention concerns molecular biological and immunodetection kits. The

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labelled nucleic acid segments, proteins or antibodies may be employed to detect other telomerase-associated nucleic acid, protein or antibody components in extracts, cells or biological samples, as may be used in the
5 detection of telomerase in clinical samples, or in the purification of telomerase-associated components, as appropriate. The kits will generally include a suitable telomerase-associated nucleic acid segment or antibody together with an detection reagent, and a means for
10 containing the telomerase-associated component and reagent.

The detection reagent will typically comprise a label associated with the telomerase nucleic acid segment
15 or antibody, or even associated with a secondary binding ligand. Exemplary ligands include secondary antibodies directed against a first antibody. The kits may contain telomerase-associated nucleic acid segments or antibodies either in fully conjugated form, in the form of
20 intermediates, or as separate moieties to be conjugated by the user of the kit.

Kits for use in molecular biological tests to identify telomerase-associated components may also
25 contain one or more unrelated nucleic acid probes or primers for use as controls, and optionally, one or more further molecular biological reagents, such as restriction enzymes or PCR components. The components of the kits will preferably be packaged within distinct
30 containers.

The container means for any of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which the
35 nucleic acid or antibody may be placed, and preferably suitably allocated. Where a second component, e.g., a binding ligand is provided, the kit will also generally

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contain a second vial or other container into which this ligand or antibody may be placed. The kits of the present invention will also typically include a means for containing the vials in close confinement for commercial sale, such as, e.g., injection or blow-molded plastic containers into which the desired vials are retained.

D. Telomerase-Associated Methods

The invention further provides methods for detecting non-ciliate eukaryotic, and preferably, yeast telomerase-associated genes or nucleic acid segments in samples, such as cells, cellular extracts, partially purified telomerase compositions and other biological and even clinical samples. Such methods generally comprise obtaining sample nucleic acids from a sample suspected of containing a telomerase-associated gene; contacting the sample nucleic acids with a telomerase-associated nucleic acid segment as described herein under conditions effective to allow hybridization of substantially complementary nucleic acids; and detecting the hybridized complementary nucleic acids thus formed.

A variety of hybridization techniques and systems are known that can be used in connection with the telomerase detection aspects of the invention. For example, *in situ* hybridization, Southern blotting, Northern blotting and PCR technology. *In situ* hybridization describes the techniques wherein the target nucleic acids contacted with the probe sequences are located within one or more cells, such as cells within a clinical sample or cells grown in culture. As is well known in the art, the cells may be prepared for hybridization by fixation, e.g. chemical fixation, and placed in conditions that allow for the hybridization of a detectable probe with nucleic acids located within the fixed cell.

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Alternatively, target nucleic acids may be separated from a cell or clinical sample prior to contact with a probe. Any of the wide variety of methods for isolating target nucleic acids may be employed, such as cesium
5 chloride gradient centrifugation, chromatography (e.g., ion, affinity, magnetic), phenol extraction and the like. Most often, the isolated nucleic acids will be separated, e.g., by size, using electrophoretic separation, followed by immobilization onto a solid matrix, prior to contact
10 with the labelled probe. These prior separation techniques are frequently employed in the art and are generally encompassed by the terms "Southern blotting", that detects DNA and "Northern blotting", that detects RNA. Virtually of the methods may be adapted for
15 clinical or diagnostic assays, including diagnostic PCR technology.

In general, the "detection" of telomerase sequences is accomplished by attaching or incorporating a
20 detectable label into the nucleic acid segment used as a probe and "contacting" a sample with the labeled probe. In such processes, an effective amount of a nucleic acid segment that comprises a detectable label (a probe), is brought into direct juxtaposition with a composition
25 containing target nucleic acids. Hybridized nucleic acid complexes may then be identified by detecting the presence of the label, for example, by detecting a radio, enzymatic, fluorescent, or chemiluminescent label.

30 These detection methods may be employed to detect telomerase-associated genes, whether RNA- or protein-encoding, in both clinical and laboratory samples, e.g., as may be used in telomerase purification, analysis, mutagenesis and the like. In cells or cellular extracts
35 obtained from an animal or human patient, the detection of telomerase may have particular relevance, for example, in the diagnosis or detection of tumor cells within a

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sample suspected of containing such cells. This is supported by recent findings linking telomerase to oncogenesis and various late stage tumors and tumor cells (Harley et al., 1992; Counter et al., 1992, 1994a; Shay et al., 1993; Klingelutz et al., 1994; de Lange, 1994; Greider, 1994). The differential detection and diagnosis of malignant tumors as opposed to benign tumors is also contemplated.

Further clinical samples that may be analyzed for the presence of telomerase-associated genes, as described above, include those suspected of containing a pathogen. As telomerase activity is only present in dividing cells, testing a sample of somatic cells of an animal or human for the presence of telomerase may indicate the presence of an invading unicellular organism within the sample. This may allow disease diagnosis alone, or in combination with other methods. The diagnosis of yeast infections, for example, is an immediate application of the present invention. The development of species-specific markers for other opportunistic infections is also contemplated.

Diagnostic methods for identifying various conditions associated with infertility in animals and humans are also provided by the invention. For example, as telomerase activity is required in germ cells, including human sperm and ova, testing samples from animals and humans suspected of having a condition connected with reproductive failure would provide useful information. A negative test would likely indicate a defect in the reproductive capacity of sperm or egg cells within a given sample.

In further embodiments, the invention concerns methods based upon suppression of "telomeric silencing" for use in identifying non-ciliate, and preferably, yeast telomerase-associated genes or active fragments thereof.

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Such methods generally comprise, initially, preparing a cell containing a chromosome that contains a genetic marker located proximal to a telomere, wherein the telomere represses the expression of the marker. Next, one would contact the cell with a composition comprising a candidate gene and identify any gene, or portion thereof, that allows expression of the marker. "Genes" identified in this way may be wild type genes or fragments that may disrupt the telomere function due to over-expression, or they may be mutant or truncated genes that simply do not function correctly.

Appropriate cells for use in such assays include those cells that contain an active telomere, such as eukaryotic cells that are capable of dividing, as exemplified by yeast cells, drosophila cells, and certain human cells, such as sperm, egg and cancer cells. The novel technology developed by the inventors is contemplated for use in any organism in which the telomeres cause a transcriptional repression (silencing) of nearby genes. For ease of operation, yeast and *Drosophila melanogaster* (fruit flies) are currently preferred. However, the use of human cells is also contemplated.

The genetic markers that are added in the vicinity of a telomere may be any marker gene that gives a readily identifiable phenotype upon expression. Such markers are also often termed "reporter genes". Generally, the marker or reporter genes encode a polypeptide not otherwise produced by the cell which is detectable by analysis, e.g., by visual inspection or by fluorometric, radioisotopic or spectrophotometric analysis. One example is *E. coli* beta-galactosidase, which produces a color change upon cleavage of an indigogenic substrate; a further example is the enzyme chloramphenicol acetyltransferase (CAT), which may be employed with a

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variety of substrates that give detectable products; and still further examples are firefly and bacterial luciferases.

5 Still further marker genes for use herewith are those capable of transforming the host cell to express unique cell surface antigens, e.g., viral env proteins such as HIV gp120 or herpes gD, which are readily
10 detectable by immunoassays. The polypeptide products of this type of marker gene are secreted, membrane bound polypeptides, or polypeptides adapted to be membrane
15 targeted, allowing ready detection by antibodies. However, antigenic reporters are not currently preferred because, unlike enzymes, they are not catalytic and thus
do not amplify their signals.

 Yeast markers, when expressed, may result in a colored phenotype or result in a specific nutrient
independence (prototrophy), or even in a nutrient
20 requirement, or such like. Exemplary genetic markers that may be used in yeast include genes that are required for the biosynthesis of specific amino acids, such as
25 *HIS3*, *TRP1*, *LYS2*, and *LEU2*. Genes that confer sensitivity to drugs, such as the *CAN1* gene that confers sensitivity to canavanine are also contemplated for use.
Currently preferred marker genes for use in yeast are
ADE2 and *URA3*.

 Many suitable genetic markers are also available for
30 use in human cell systems. These include the markers based upon color detection or antigen detection, as above, and also marker genes that encode polypeptides, generally enzymes, that render the host cells resistant
35 against toxins. These include the *neo* gene that protects host cells against toxic levels of the antibiotic G418; the dihydrofolate reductase genes that confer resistance to methotrexate; and the HSV tk gene that is used in

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conjunction with ganciclovir. Currently preferred examples are the markers *neo* and *hprt*, which are routinely used in the art.

5 The cells used in such assays may contain two distinct genetic markers, and each genetic marker may be located on a distinct chromosome if desired. The combined use of *ADE2* and *URA3* in yeast cells is currently a particularly preferred system.

10 As described hereinabove, human telomerase RNA template and polypeptide-encoding genes that have substantial sequence homology to the yeast sequences throughout, or in certain sequence regions, may be
15 isolated by nucleic acid hybridization, i.e., standard cloning techniques (Sambrook et. al., 1989). However, even if the human sequences are not directly homologous, RNA template and other telomerase genes may still be isolated using the advantageous methods disclosed herein.

20 One suitable method for identifying a human telomerase-associated gene, is to apply the suppression of telomeric silencing protocol to a human nucleic acid library using a yeast cell system. Such methods
25 generally comprise preparing a yeast cell containing a chromosome that contains a genetic marker located proximal to a telomere, where the telomere represses the expression of the marker; contacting the cell with a composition comprising a candidate human gene; and
30 identifying a human gene that allows expression of the marker.

35 Further suitable methods for identifying human telomerase-associated genes are those based entirely upon human cells, which methods presuppose the lowest level of homology between the yeast and human cell systems. These methods comprise preparing a human cell that contains a

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chromosome having a genetic marker located proximal to a telomere, where the telomere represses the expression of the marker; contacting the cell with a composition comprising a candidate human gene; and identifying a human gene that allows expression of the marker.

Another method for isolating genes that encode products that interact with telomerase RNA is that which assays for genes that re-establish telomeric silencing when the template RNA is overexpressed, as described in Example XIV. Here, initially the RNA template is presumed to interact with a limiting telomerase component to form a non-functional complex. Increasing the concentration of a limiting component, by over-expression, thus re-establishes telomeric silencing. Preferably, RNA template levels that are minimally suppressive are used.

Still more approaches for identifying components that interact with telomerase RNA are described in Example XIV, which are based upon isolating mutations that enhance or suppress the phenotypes of conditional telomerase template alleles.

Further elements of this invention are non-ciliate eukaryotic, and preferably, yeast genes that are identified by any of the foregoing methods. One such gene is disclosed herein, termed *TLC1*, that encodes a telomerase RNA template. Other such genes are also disclosed herein, termed *STR* genes, that encode telomerase-associated polypeptides. Particular examples of such genes of the invention are thus *TLC1*, *STR1*, *STR3*, *STR4*, *STR5* and *STR6*, and other non-ciliate eukaryotic, and preferably, yeast nucleic acid segments that have the physical and functional characteristics of any of the foregoing genes.

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Active fragments of genes and RNA components, such as *TLC1* RNA, may also be identified using the present methods. Titration assays based upon those used for the original identification of *TLC1* may be used to define the minimum functional region. It is contemplated that relatively small regions of the RNA (about 50 bp) that suppress silencing will be identified. Conditional mutations made in regions of the RNA that are evolutionarily conserved, or that may interact with a limiting factor, as suggested by the titration analysis, will identify functionally important region of the telomerase RNA. Active regions of telomerase genes and RNA components may also be identified using methods for dissecting small nuclear RNAs (snRNAs), as described in Example XIII.

In still further embodiments, the invention provides methods for use in identifying candidate substances that bind to yeast and other non-ciliate eukaryotic telomerase components. These methods generally include preparing an isolated telomerase component; contacting the isolated telomerase component with a composition comprising a candidate substance under conditions effective and for a period of time sufficient to allow binding; and detecting the presence of a telomerase component-candidate substance bound complex.

It will be understood that such methods are similar in principle to the nucleic acid hybridization methods described hereinabove. Indeed, the "candidate substances" to be detected may be nucleic acids, including human nucleic acid segments, that are detected by binding to eukaryotic, and preferably, to yeast telomerase RNA or DNA components, and preferably to a defined small functional region of the template that suppress silencing, under the high or low hybridization conditions described above. However, other components

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that bind to telomerase may be identified by binding to the isolated RNA, DNA or polypeptide components of the present invention. These components may include proteins, polypeptides, peptides, antibodies, small
5 molecules, cofactors and the like.

Accordingly, the present invention provides binding assays, including high throughput binding assays using recombinant expression products, for use in identifying
10 compounds capable of binding to telomerase or to a telomerase-associated component. The binding assays will preferably use the smaller RNA fragments identified in titration or other functional assays described herein.

15 Further methods for identifying compounds that bind to telomerase-associated components include those based upon cellular assays. One method for identifying a candidate substance that modifies telomerase activity comprises the following steps:

20 preparing a eukaryotic, or preferably, a yeast cell containing a chromosome that contains a genetic marker located near to, or in the vicinity of, a telomere, the telomere capable of repressing the
25 expression of the marker;

contacting the cell with a composition comprising a candidate substance; and

30 identifying a candidate substance that allows expression of the marker or that further 'represses the expression of the marker.

This method is most suitable for identifying
35 candidate inhibitory substances that allow expression of the marker. However, it can also be used to identify

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candidate stimulatory substances that allow further repression of the marker.

5 To identify a compound that inhibits telomerase activity, one generally prepares a cell with a genetic marker that is substantially repressed by the telomere. Here, the marker gene is located proximal, i.e., immediately adjacent, to the telomere. Substantial repression is defined by repression to at least about 10 50%, or preferably, to about 25%, 10% or about 1%. However, the expression of the marker may be repressed to even about 0.01%. The inhibitory substance is then detected by detecting greater expression of the marker.

15 To identify a compound that activates telomerase activity, one would generally prepare a cell with a genetic marker that is either not repressed at all or that is not substantially or maximally repressed. One would then select a candidate activator by identifying a 20 substance that establishes or allows repression or more substantial repression. This is based upon the concept that stimulating telomerase to synthesize longer than normal telomeres will result in an increase in silencing of a marker gene. To detect the increase requires that a 25 system initially be established in which the marker gene is only minimally repressed, or even not repressed at all. This is readily achieved by inserting the marker gene in the location or vicinity of the telomere, but further away from the telomere rather than immediately 30 adjacent to it. An increase in repression, i.e., a decrease in marker gene expression, indicates a positive candidate substance.

35 Still further methods for identifying compounds that functionally interact with telomerase or telomerase-associated components are those based upon the telomerase "healing of broken chromosomes" assay described herein.

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This method is conducted as generally described in Example XII and FIG. 8, using a modified Haber-based assay (Kramer & Haber, 1993). Other useful telomerase functional assays are those that analyze telomere length and cell viability with increased age of a culture (Lundblad & Blackburn, 1989), and those *in vitro* systems described herein based on the addition of labelled nucleotides to a telomeric-like sequence.

Any of the cellular or activity-based telomerase assays may be adapted to screen for candidate substances that modify telomerase activity. To achieve this, one would first conduct the assay in the absence of the test candidate substance to obtain an activity value in its absence. One would then add the candidate substance to the telomerase composition or cell and conduct the assay under the same conditions. Candidate substances that reduce or promote telomerase activity can thus be readily identified.

Useful telomerase-modifying compounds are not believed to be limited in any way to protein or peptidyl compounds or oligonucleotides. In fact, it may prove to be the case that the most useful pharmacological compounds identified through application of a screening assay will be non-peptidyl in nature. Accordingly, in such screening assays, it is proposed that compounds isolated from natural sources, such as animals, bacteria, fungi, plant sources, including leaves and bark, and marine samples, may be assayed for the presence of potentially useful pharmaceutical agents. It will be understood that the pharmaceutical agents to be screened could also be derived from chemical compositions or man-made compounds.

The invention thus further encompasses components that bind to telomerase and that are capable of modifying

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telomerase activity, as may be identified by any of the foregoing binding and/or functional or cellular assay methods. This results in compositions of telomerase activators or inhibitors, including pharmaceutically acceptable compositions, and methods for modifying telomerase activity.

In yet still further embodiments, the present invention thus also provides methods for modifying the replicative capacity of a cell, which methods comprise contacting a telomerase-containing cell with an amount of a component or substance effective to modify telomerase activity. "Modifying" in this context includes both compositions and methods for inhibiting telomerase activity, as may be used, e.g., in inhibiting or killing a tumor cell or a pathogen; and compositions and methods for stimulating telomerase activity, as may be used in embodiments connected with promoting the replication of a cell, such as in treating infertility.

Where the telomerase-containing cells are located within an animal, a pharmaceutically acceptable composition of the telomerase activator or inhibitor may be administered to the animal in an amount effective to modify the telomerase activity of the target cell. In terms of inhibiting telomerase activity in tumor cells, this is contemplated to be an effective mechanism by which to treat cancer that will have very limited side effects. Similarly, effective antimicrobial treatments are contemplated, as are applications in treating age-related disorders such as atherosclerosis and osteoporosis. Further, gene therapy using functional telomerase-associated genes is envisioned to be of use in treating telomerase dysfunction, as could provide a treatment for infertility in humans and other animals.

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BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1A, FIG. 1B and FIG. 1C. Overexpression of *TLC1* suppresses transcriptional silencing at telomeres, but not at the *HML* locus. In FIG. 1A, Viability on medium lacking uracil was measured for *S. cerevisiae* strains containing *URA3* either at telomere VII-L (UCC3505) or at *HML* (UCC3515), and overexpressing either vector alone (pTRP, black bar), a representative *TLC1* cDNA clone (pTRP6, hatched bar), or a *SIR4* cDNA clone (pTRP10, white bar) (Kyrion et al., 1993). In FIG. 1B, *ADE2* expression, as assayed by colony color, was examined in cells containing *ADE2* placed near telomere V-R (UCC3505), and containing the vector (pTRP). In FIG. 1C, *ADE2* expression, as assayed by colony color, was examined in cells containing *ADE2* placed near telomere V-R (UCC3505), and containing another representative *TLC1* cDNA clone (pTRP61). The medium contained 3 % galactose and lacked tryptophan. The median value for viability in the absence of uracil is marked by the height of each column, and the upper extreme is indicated by the error bar. The strains were pregrown for four days on solid synthetic medium without tryptophan (to maintain selection for the plasmid) that contained 3 % galactose (to induce the *GAL1* promoter controlling expression of the cDNA inserts). Colonies were then diluted in water, and serial dilutions were plated on 3 % galactose medium without tryptophan and uracil. Cells were also plated on medium containing uracil, to determine overall cell viability. Five independent transformants of each strain were tested.

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FIG. 2. Overexpression of *TLC1* causes a decrease in telomeric tract length. Yeast strain UCC3505 carrying either vector (pTRP, lanes 1 and 2) or a *TLC1* cDNA clone (pTRP6, lanes 3 and 4) were pregrown for approximately 60 generations on medium containing 3 % galactose without tryptophan. Genomic DNA was prepared from two independent transformants of each strain, digested with *Apa* I and *Xho* I, separated by electrophoresis on a 1 % agarose gel, and blotted onto a nylon membrane. The membrane was probed with a 1.1 kb *Hind* III-*Sma* I *URA3* fragment. The *URA3* gene in this strain is located adjacent to telomere VII-L. The higher molecular weight (non-telomeric) *URA3* fragments represent sequences of the telomeric *URA3* that are centromere-proximal to the *URA3* *Apa* I site, and sequences from the *ura3-52* allele at the normal chromosomal locus of *URA3*. The Southern blot was also probed with an 81 bp labeled (TG)₁₋₃TG₂₋₃ (telomeric sequence) riboprobe, to determine the telomere length of chromosomes with Y' elements (Walmsey et al., 1984). These telomere-associated sequences are at the ends of multiple yeast chromosomes and generally have *Xho* I sites at their telomere-proximal ends (Louis & Haber, 1990). Y'-containing chromosomes showed a decrease of telomere length upon overexpression of the *TLC1* cDNA clone similar to that seen for telomere VII-L.

FIG. 3A and FIG. 3B. *TLC1* encodes a 1.3 kb RNA. *TLC1* transcript levels were analyzed in yeast strains containing a wild-type *TLC1* gene (lane 1), or a *tlc1::LEU2* disruption allele (lane 2), and in wild-type cells carrying either vector (pTRP, lane 3) or a *TLC1* cDNA clone (pTRP61, lane 4). Total RNA was isolated from mid-log phase cells grown in rich medium (for strains lacking plasmids) or synthetic medium without tryptophan but with 3 % galactose (for the plasmid-containing strains). 20 µg of RNA from each strain was electrophoretically separated on a 0.9 % agarose

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formaldehyde gel and transferred to a nylon membrane. FIG. 3A shows the membrane probed with a 1.25 kb *TLC1* antisense probe (made from the pTRP61 insert) and exposed to film. Phosphor-imaging analysis determined that there is approximately 12-fold more *TLC1* RNA in the overexpressing strain (lane 4) than in the vector-containing wild-type strain grown under the same conditions (lane 3). FIG. 3B displays the ethidium bromide-stained gel prior to blotting, with the sizes of the rRNA species (25S and 18S) indicated on the right. The wild-type and *tlc1* strains shown in lanes 1 and 2 were derived from sporulation of UCC3508 (Aparicio et al., 1991). The yeast strain transformed with the pTRP and pTRP61 plasmids, shown in lanes 3 and 4, is UCC3505.

FIG. 4A. Disruption of *TLC1* causes progressive telomere shortening and a gradual decrease in growth rate and viability. A *TLC1/tlc1::LEU2* diploid (UCC3508) was sporulated and the resulting tetrads dissected and germinated on rich medium. Colonies representing the four spore products from a tetrad were inoculated into 5.5 ml of rich medium and grown at 30°C. Every 24 hours, 5 ml of the culture were used for the preparation of genomic DNA, and 5 µl were used to inoculate 5.5 ml of fresh medium. The genomic DNA was digested with *Apa* I, electrophoresed on a 1 % agarose gel, transferred to a nylon membrane and hybridized to a 1.1 kb *URA3* probe. The *URA3* gene is located adjacent to telomere VII-L in these strains. In a similar study, genomic DNA from *TLC1* and *tlc1* cultures was digested with *Xho* I, as well as *Apa* I, in order to examine Y'-containing telomeres using the Southern blotting method described in FIG. 2 with the 81 bp labeled telomeric sequence riboprobe (Walmsey et al., 1984). The size of this population of telomeres decreased in size at the same rate as the *URA3*-labeled telomere VII-L.

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FIG. 4B. Disruption of *TLC1* causes progressive telomere shortening and a gradual decrease in growth rate and viability. In a study similar to that of FIG. 4A, UCC3508 spore products were grown continuously in rich medium. Every 24 hours the cell density was determined and each culture was diluted to 3×10^5 cells/ml in 5.5 ml of fresh medium for further growth. The cell density at each time point is plotted for the two *TLC1* (white circle and square) and *tlc1* (black circle and square) spore products of a tetrad.

FIG. 5A and FIG. 5B. The *TLC1* gene encodes an RNA that functions as a templating component of telomerase, an enzyme that elongates the G-rich strand of *S. cerevisiae* telomeres. In FIG. 5A, is shown a model by which the *TLC1* RNA anneals to the single-stranded G-rich overhanging strand at the end of the chromosome and templates its elongation via a reverse transcription reaction. The bold-type DNA bases represent newly synthesized sequence. FIG. 5B, shows that, accordingly, mutating the putative template motif of *TLC1*, creating the *TLC1-1(HaeIII)* allele, results in the incorporation of the altered sequence into telomeric DNA.

FIG. 6A. Altering the putative telomere-templating region of *TLC1* results in the incorporation of the mutant sequence into telomeric tracts. Fragment-mediated transformation of *TLC1/TLC1* and *TLC1-1(HaeIII)/TLC1* diploid strains was used to replace the terminal sequences of the left arm of one of the chromosome VII homologs with a *URA3* gene and a short telomeric tract sequence. The most telomere-proximal *Apa I* and *Hae III* sites in the fragment used in the transformation overlap and are located 0.75 kb from the telomeric end of the fragment.

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FIG. 6B. Altering the putative telomere-templating region of *TLC1* results in the incorporation of the mutant sequence into telomeric tracts. Restriction digests of genomic DNA from transformed strains were used to
5 determine whether Hae III sites were introduced into the new telomere VII-L upon its elongation *in vivo*. Genomic DNA from *TLC1/TLC1* and *TLC1-1(HaeIII)/TLC1* yeast strains, either transformed with *URA3TEL* (Telomeric *URA3+*) or not (Telomeric *URA3-*), was digested with Apa I (A) or Hae III
10 (H). The DNA fragments were separated by electrophoresis on a 1.25 % agarose gel, transferred to a nylon membrane, and probed with a labeled 0.6 kb *URA3* probe (Apa I-Hind III fragment), as depicted in FIG. 6A. Each Telomeric *URA3+* strain represents an independently isolated
15 transformant.

FIG. 7A. Quantitative suppression of telomeric silencing by various different genes. This was assessed by viability in the absence of uracil for the strains that
20 contained the telomeric *URA3* gene and each of the 10 highly expressed genes of Example X. All the genes suppressed silencing of the telomeric *URA3*, although a hierarchy of suppression was observed.

FIG. 7B. Effect of genes on silencing at *HML*. The expression plasmids containing each of the 10 genes of Example X were introduced into a strain in which the *URA3* gene was inserted into the *HML* locus (Mahoney & Broach, 1989). Overexpression of *TLC1* (*STR2*) had no effect on
25 silencing at *HML*, but strongly suppressed telomeric silencing of *URA3* and *ADE2*. The *SIR4* and *ASF1* genes derepressed *HML* very well, as did the *STR1*, *STR4*, and *RRP3* genes. Overexpression of *RPL32*, *STR3*, *STR5* and *STR6*
30 had intermediate effects at *HML*.

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FIG. 8. Schematic representation of the new genetic system to test telomere healing, as described in Section 2 of Example XII.

5 DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Telomeres, the natural ends of linear eukaryotic chromosomes, are essential for chromosome stability. Because of the nature of DNA replication, telomeres
10 require a specialized mechanism to ensure their complete duplication. This is controlled by telomerase activity. Due to its role in controlling replication, changes in telomerase activity have been linked to disturbances in cell proliferation, as can lead to a cancerous phenotype
15 (de Lange, 1994; Greider, 1994; Harley et al., 1992).

The evolutionary conservation of telomere structure suggested to the present inventors that the study of telomerase in genetically tractable organisms, such as
20 the budding yeast *Saccharomyces cerevisiae*, would yield important information directly applicable to telomere studies in eukaryotic and mammalian cells. The existence of an *S. cerevisiae* telomerase was suggested by studies in which double-strand breaks were introduced into yeast
25 chromosomes *in vivo*, after which healed chromosomes with new telomeric tracts were formed (Kramer & Haber, 1993). Specific 13-bp motifs (GTGTGTGGGTGTG; SEQ ID NO:2), or subsets thereof, were found at the junction between the break site and the new telomeric tracts, suggesting that
30 this sequence is added *de novo* (Kramer & Haber, 1993).

However, prior to the present invention, little was known about the molecular machinery that could be involved in telomeric replication in *S. cerevisiae*.
35 Previously, the only candidate as a component of the telomere replication apparatus was the protein encoded by the *EST1* gene (Lundblad & Szostak, 1989). Its role in

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telomere replication was suggested by the finding that
est1 cells display progressive telomere shortening,
accompanied by a gradual loss of chromosome stability and
cell viability. The direct function of Est1p still
5 remains to be elucidated.

The inventors discovered that *S. cerevisiae*
telomeres repress, or silence, expression of genes
located nearby (Example I). Silencing of telomeric genes
10 is due to a structurally distinct chromatin domain whose
formation initiates at the telomere (Example III).
Evidence for this specialized chromatin structure
includes: identification of mutations in the histone H3
and H4 genes which relieve telomeric silencing (Example
15 II), the finding that telomere-adjacent chromatin
contains histone H4 in a hypoacetylated state compared to
H4 in actively transcribed chromatin (Braunstein et al.,
1993), and the relative inaccessibility of
telomere-proximal DNA to *in vivo* modification by the
20 *E. coli* dam methyltransferase protein (Gottschling,
1992). At least six additional gene products, including
the telomere DNA binding protein, RAP1, are required for
telomeric silencing (Aparicio et al., 1991; Kyrion
et al., 1993).

25

In order to identify genes in *S. cerevisiae* that are
important for telomere function, the inventors developed
and used a novel screening method to identify genes that,
when expressed at high levels, suppress telomeric
30 silencing. This screen lead to the identification of the
gene *TLC1* (telomerase component 1), one of the components
of the present invention, along with several other novel
genes.

35

TLC1 encodes the template RNA of telomerase, a
ribonucleoprotein required for telomere replication in a
variety of organisms. The discovery of *TLC1* is the first

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clear evidence that shows telomerase exists in
S. cerevisiae. This finding will facilitate further
telomerase studies and screening assays to identify
activators or inhibitors with potential for modulating
5 telomerase activity, as may ultimately be used in a
clinical setting.

The present discoveries may be utilized in
conjunction with certain techniques that are well-known
10 in the biological arts and that are further described in
the following sections.

A. Biological Functional Equivalents

15 Modification and changes may be made in the
structure of telomerase-associated polypeptides and still
obtain molecules having like or otherwise desirable
characteristics. For example, certain amino acids may be
substituted for other amino acids in a protein structure
20 without appreciable loss of interactive binding capacity
with structures such as, for example, antigen-binding
regions of antibodies or binding sites on substrate
molecules, receptors, RNA molecules, chromosomal ends and
the like. Since it is the interactive capacity and
25 nature of a protein that defines that protein's
biological functional activity, certain amino acid
sequence substitutions can be made in a protein sequence
(or, of course, its underlying DNA coding sequence) and
nevertheless obtain a protein with like (agonistic)
30 properties. Equally, the same considerations may be
employed to create a protein or polypeptide with
countervailing (e.g., antagonistic) properties. It is
thus contemplated by the inventors that various changes
may be made in the sequences of the telomerase-associated
35 proteins or peptides disclosed herein (or their
underlying DNA) without appreciable loss of their
biological utility or activity.

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It is also well understood by the skilled artisan that, inherent in the definition of a biologically functional equivalent protein or peptide, is the concept that there is a limit to the number of changes that may be made within a defined portion of the molecule and still result in a molecule with an acceptable level of equivalent biological activity. Biologically functional equivalent peptides are thus defined herein as those peptides in which certain, not most or all, of the amino acids may be substituted. In particular, where smaller peptides are concerned, it is contemplated that relatively few amino acids may be changed within a given peptide. Of course, a plurality of distinct proteins/peptides with different substitutions may easily be made and used in accordance with the invention.

It is also well understood that where certain residues are shown to be particularly important to the biological or structural properties of a protein or peptide, e.g., residues in active sites or key binding regions, such residues may not generally be exchanged.

Amino acid substitutions are generally based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. An analysis of the size, shape and type of the amino acid side-chain substituents reveals that arginine, lysine and histidine are all positively charged residues; that alanine, glycine and serine are all a similar size; and that phenylalanine, tryptophan and tyrosine all have a generally similar shape. Therefore, based upon these considerations, arginine, lysine and histidine; alanine, glycine and serine; and phenylalanine, tryptophan and tyrosine; are defined herein as biologically functional equivalents.

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To effect more quantitative changes, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these
5 are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3);
10 proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

The importance of the hydropathic amino acid index in conferring interactive biological function on a
15 protein is generally understood in the art (Kyte & Doolittle, 1982, incorporated herein by reference). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In
20 making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

25

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the
30 greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e. with a biological property of the protein. Thus, it is understood that an amino acid can
35 be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent protein.

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As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine
5 (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 \pm 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

10

In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those
15 within ± 0.5 are even more particularly preferred.

While discussion has focused on functionally equivalent polypeptides arising from amino acid changes, it will be appreciated that these changes may be effected
20 by alteration of the encoding DNA; taking into consideration also that the genetic code is degenerate and that two or more codons may code for the same amino acid. A table of amino acids and their codons is presented herein (Table 1) for use in such embodiments,
25 as well as for other uses, such as in the design of probes and primers and the like.

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TABLE 1

<u>Amino Acids</u>				<u>Codons</u>					
5	Alanine	Ala	A	GCA	GCC	GCG	GCU		
	Cysteine	Cys	C	UGC	UGU				
	Aspartic acid	Asp	D	GAC	GAU				
	Glutamic acid	Glu	E	GAA	GAG				
	Phenylalanine	Phe	F	UUC	UUU				
10	Glycine	Gly	G	GGA	GGC	GGG	GGU		
	Histidine	His	H	CAC	CAU				
	Isoleucine	Ile	I	AUA	AUC	AUU			
	Lysine	Lys	K	AAA	AAG				
	Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
15	Methionine	Met	M	AUG					
	Asparagine	Asn	N	AAC	AAU				
	Proline	Pro	P	CCA	CCC	CCG	CCU		
	Glutamine	Gln	Q	CAA	CAG				
	Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
20	Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
	Threonine	Thr	T	ACA	ACC	ACG	ACU		
	Valine	Val	V	GUA	GUC	GUG	GUU		
	Tryptophan	Trp	W	UGG					
	Tyrosine	Tyr	Y	UAC	UAU				

25

In addition to the peptidyl compounds described herein, the inventors also contemplate that other sterically similar compounds may be formulated to mimic the key portions of the peptide structure. Such compounds, which may be termed peptidomimetics, may be used in the same manner as the peptides of the invention and hence are also functional equivalents. The generation of a structural functional equivalent may be

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achieved by the techniques of modelling and chemical design known to those of skill in the art. It will be understood that all such sterically similar constructs fall within the scope of the present invention.

5

U.S. Patent 4,554,101 (Hopp, incorporated herein by reference) also teaches the identification and preparation of epitopes from primary amino acid sequences on the basis of hydrophilicity. Through the methods disclosed in Hopp one of skill in the art would be able to identify epitopes from within the telomerase-associated amino acid sequences disclosed herein. Such regions would also be referred to as "eptiopic core regions".

15

Numerous scientific publications have been devoted to the prediction of secondary structure, and to the identification of epitopes, from analyses of amino acid sequences (Chou & Fasman, 1974a,b; 1978a,b, 1979). Any of these may be used, if desired, to supplement the teachings of Hopp in U.S. Patent 4,554,101. Moreover, computer programs are currently available to assist with predicting antigenic portions and eptiopic core regions of proteins. Examples include those programs based upon the Jameson-Wolf analysis (Jameson & Wolf, 1998; Wolf et al., 1988), the program PepPlot® (Brutlag et al., 1990; Weinberger et al., 1985), and other new programs for protein tertiary structure prediction (Fetrow & Bryant, 1993). The identification of epitopic regions from within the telomerase-associated sequences allows the ready generation of specific antibodies.

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B. Site-Specific Mutagenesis

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Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, through

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specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart the two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes a telomerase-associated component. An oligonucleotide primer bearing the desired mutated sequence is prepared, this primer is then annealed with the single-stranded vector, and subjected

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to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-
5 mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

10 The preparation of sequence variants of the selected telomerase-associated gene using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be
15 limiting as there are other ways in which sequence variants may be obtained. For example, recombinant vectors encoding a desired telomerase-associated gene may be treated with mutagenic agents to obtain sequence variants, as used in the mutagenesis of plasmid DNA using
20 hydroxylamine.

C. Nucleic Acid Hybridization

In Southern analysis, membrane-bound, denatured DNA
25 fragments are hybridized to a labeled DNA probe. Following this hybridization, the membrane is washed in order to remove nonspecifically bound probe, leaving only probe that is specifically base-paired to the target DNA. By controlling the stringency of the washing conditions,
30 different levels of probe-target DNA complementarity may be detected.

High stringency conditions are useful in order to identify DNA fragments with little mismatch, even close
35 to and including 100% complementarity to the probe DNA. Low stringency conditions are used to identify sequences that are related, though not identical, to the probe DNA,

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e.g., members of a multigene family, or a single gene in a different organism.

Preferred hybridization conditions are, currently,
5 those that use a buffer of 5x SSC, 0.5%(w/v) blocking
reagent, 0.1% (w/v) N-lauroylsarcosine, Na-salt,
0.02%(w/v) SDS and 50% (w/v) formamide, with
hybridization at 42°C overnight. The high stringency
washing conditions involve washing the blot twice for 5
10 minutes with Blot Wash #1 (2x SSC, 0.1% (w/v) SDS), and
then washing twice for 15 minutes with Blot Wash #2 (0.1x
SSC, 0.1% (w/v) SDS) at 55°C.

For low stringency hybridization, the hybridization
15 conditions remain using 5x SSC, 0.5%(w/v) blocking
reagent, 0.1% (w/v) N-lauroylsarcosine, Na-salt,
0.02%(w/v) SDS and 50% (w/v) formamide, with
hybridization at 42°C overnight. The low stringency
washing conditions involve using Blot wash #2 as
20 0.2x SSC, 0.1% (w/v) SDS at 45°C. In the low stringency
protocols, a certain limited variation in the conditions
may be necessary to achieve optimal conditions, on a
case-by-case basis. Such optimization is standard and
routinely practiced by those of skill in the art.

25

D. Protein Expression

To express a recombinant telomerase-associated RNA
or protein component in accordance with the present
30 invention one would prepare an expression vector that
comprises the telomerase-associated component under the
control of one or more promoters. The "upstream"
promoters stimulate transcription of the DNA and promote
expression of the encoded recombinant protein or RNA
35 unit. This is the meaning of "recombinant expression" in
this context.

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Many standard techniques are available to construct expression vectors containing the appropriate nucleic acids and transcriptional/translational control sequences in order to achieve RNA or protein expression in a variety of host-expression systems. Cell types available for expression include, but are not limited to, bacteria, such as *E. coli* and *B. subtilis* transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors.

10

Certain examples of prokaryotic hosts are *E. coli* strain RR1, *E. coli* LE392, *E. coli* B, *E. coli* X 1776 (ATCC No. 31537) as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325); bacilli such as *Bacillus subtilis*; and other enterobacteriaceae such as *Salmonella typhimurium*, *Serratia marcescens*, and various *Pseudomonas* species.

15

In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is often transformed using pBR322, a plasmid derived from an *E. coli* species. pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microbial organism for expression of its own proteins.

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In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as transforming vectors in connection with these hosts. For example, the phage

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lambda GEMTM-11 may be utilized in making a recombinant phage vector which can be used to transform host cells, such as *E. coli* LE392. Further useful vectors include pIN vectors; and pGEX vectors, for use in generating
5 glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

Those promoters most commonly used in recombinant DNA construction include the β -lactamase (penicillinase),
10 lactose and tryptophan (*trp*) promoter systems. While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them
15 functionally with plasmid vectors.

Naturally, in certain embodiments, yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing telomerase-associated RNA
20 or protein coding sequences will be preferred in certain embodiments.

For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb et al., 1979;
25 Kingsman et al., 1979; Tschemper et al., 1980). This plasmid already contains the *trp1* gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the *trp1* lesion
30 as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors
35 include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., 1980) or other glycolytic enzymes (Hess et al., 1968; Holland et al., 1978), such as enolase,

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glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose
5 isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination.
10 Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the
15 aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization.

In yeast, any plasmid vector containing a yeast-compatible promoter, an origin of replication, and termination sequences is suitable. However, preferred recombinant expression vectors include pYPGE-2, as described by Brunelli & Pall (1993).

25 In addition to microorganisms, cultures of cells derived from multicellular organisms may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. In addition to mammalian cells, these include insect cell
30 systems infected with recombinant virus expression vectors (e.g., baculovirus); and plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression
35 vectors (e.g., Ti plasmid) containing the telomerase-associated coding sequences.

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In a useful insect system, *Autographa californica* nuclear polyhidrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The telomerase-associated protein or RNA coding sequences are cloned into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of the coding sequences results in the inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed (e.g., U.S. Patent No. 4,215,051 (Smith)).

Examples of useful mammalian host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, W138, BHK, COS-7, 293, HepG2, 3T3, RIN and MDCK cell lines. In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins. Appropriate cells lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used.

Expression vectors for use in such cells ordinarily include an origin of replication (as necessary), a

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promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences. The origin of replication may be provided either by construction of the vector to include an exogenous origin, such as may be derived from SV40 or other viral (e.g., Polyoma, Adeno, VSV, BPV) source, or may be provided by the host cell chromosomal replication mechanism. If the vector is integrated into the host cell chromosome, the latter is often sufficient.

The promoters may be derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Further, it is also possible, and often desirable, to utilize promoter or control sequences normally associated with the desired gene sequence, provided such control sequences are compatible with the host cell systems.

A number of viral based expression systems may be utilized, for example, commonly used promoters are derived from polyoma, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The early and late promoters of SV40 virus are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication. Smaller or larger SV40 fragments may also be used, provided there is included the approximately 250 bp sequence extending from the Hind III site toward the Bgl I site located in the viral origin of replication.

In cases where an adenovirus is used as an expression vector, the coding sequences may be ligated to an adenovirus transcription/ translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus

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genome by *in vitro* or *in vivo* recombination. Insertion
in a non-essential region of the viral genome (e.g.,
region E1 or E3) will result in a recombinant virus that
is viable and capable of expressing telomerase-associated
5 RNA or proteins in infected hosts.

Specific initiation signals may also be required for
efficient translation of telomerase-associated component
coding sequences. These signals include the ATG
10 initiation codon and adjacent sequences. Exogenous
translational control signals, including the ATG
initiation codon, may additionally need to be provided.
One of ordinary skill in the art would readily be capable
of determining this and providing the necessary signals.
15 It is well known that the initiation codon must be in
phase (or in-frame) with the reading frame of the desired
coding sequence to ensure translation of the entire
insert. These exogenous translational control signals
and initiation codons can be of a variety of origins,
20 both natural and synthetic. The efficiency of expression
may be enhanced by the inclusion of appropriate
transcription enhancer elements, transcription
terminators.

25 For long-term, high-yield production of recombinant
proteins, stable expression is preferred. For example,
cell lines that stably express constructs encoding
telomerase-associated components may be engineered.
Rather than using expression vectors that contain viral
30 origins of replication, host cells can be transformed
with vectors controlled by appropriate expression control
elements (e.g., promoter, enhancer, sequences,
transcription terminators, polyadenylation sites, etc.),
and a selectable marker. Following the introduction of
35 foreign DNA, engineered cells may be allowed to grow for
1-2 days in an enriched media, and then are switched to a
selective media. The selectable marker in the

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recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines.

5

A number of selection systems may be used, including, but not limited, to the herpes simplex virus thymidine kinase, hypoxanthine-guanine phosphoriboxyltransferase and adenine phosphoriboxyltransferase, in tk-, hgprt- or aprt-cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, that confers resistance to methotrexate; gpt, that confers resistance to mycophenolic acid, neo, that confers resistance to the aminoglycoside G-418; and hygromycin, that confers resistance to hygromycin.

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E. Monoclonal Antibody Generation

Means for preparing and characterizing antibodies are well known in the art (See, e.g., Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988; incorporated herein by reference).

20

The methods for generating monoclonal antibodies (MAbs) generally begin along the same lines as those for preparing polyclonal antibodies. Briefly, a polyclonal antibody is prepared by immunizing an animal with an immunogenic composition in accordance with the present invention and collecting antisera from that immunized animal. A wide range of animal species can be used for the production of antisera. Typically the animal used for production of anti-antisera is a rabbit, a mouse, a rat, a hamster, a guinea pig or a goat. Because of the relatively large blood volume of rabbits, a rabbit is a preferred choice for production of polyclonal antibodies.

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As is well known in the art, a given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as may be achieved by coupling a peptide or polypeptide immunogen to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin or rabbit serum albumin can also be used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include glutaraldehyde, m-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide and bis-biazotized benzidine.

As is also well known in the art, the immunogenicity of a particular immunogen composition can be enhanced by the use of non-specific stimulators of the immune response, known as adjuvants. Exemplary and preferred adjuvants include complete Freund's adjuvant (a non-specific stimulator of the immune response containing killed *Mycobacterium tuberculosis*), incomplete Freund's adjuvants and aluminum hydroxide adjuvant.

The amount of immunogen composition used in the production of polyclonal antibodies varies upon the nature of the immunogen as well as the animal used for immunization. A variety of routes can be used to administer the immunogen (subcutaneous, intramuscular, intradermal, intravenous and intraperitoneal). The production of polyclonal antibodies may be monitored by sampling blood of the immunized animal at various points following immunization. A second, booster injection, may also be given. The process of boosting and titering is repeated until a suitable titer is achieved. When a desired level of immunogenicity is obtained, the immunized animal can be bled and the serum isolated and stored, and/or the animal can be used to generate MAbs.

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MABs may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Patent 4,196,265, incorporated herein by reference. Typically, this technique involves immunizing a suitable
5 animal with a selected immunogen composition, e.g., a purified or partially purified telomerase-associated protein, polypeptide or peptide. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice
10 and rats are preferred animals, however, the use of rabbit, sheep frog cells is also possible. The use of rats may provide certain advantages (Goding, 1986, pp. 60-61), but mice are preferred, with the BALB/c mouse being most preferred as this is most routinely used and
15 generally gives a higher percentage of stable fusions.

Following immunization, somatic cells with the potential for producing antibodies, specifically B lymphocytes (B cells), are selected for use in the MAB
20 generating protocol. These cells may be obtained from biopsied spleens, tonsils or lymph nodes, or from a peripheral blood sample. Spleen cells and peripheral blood cells are preferred, the former because they are a rich source of antibody-producing cells that are in the
25 dividing plasmablast stage, and the latter because peripheral blood is easily accessible. Often, a panel of animals will have been immunized and the spleen of animal with the highest antibody titer will be removed and the spleen lymphocytes obtained by homogenizing the spleen
30 with a syringe. Typically, a spleen from an immunized mouse contains approximately 5×10^7 to 2×10^8 lymphocytes.

The antibody-producing B lymphocytes from the
35 immunized animal are then fused with cells of an immortal myeloma cell, generally one of the same species as the animal that was immunized. Myeloma cell lines suited for

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use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas).

Any one of a number of myeloma cells may be used, as are known to those of skill in the art (Goding, pp. 65-66, 1986; Campbell, pp. 75-83, 1984). For example, where the immunized animal is a mouse, one may use P3-X63/Ag8, X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XX0 Bul; for rats, one may use R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210; and U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6 are all useful in connection with human cell fusions.

One preferred murine myeloma cell is the NS-1 myeloma cell line (also termed P3-NS-1-Ag4-1), which is readily available from the NIGMS Human Genetic Mutant Cell Repository by requesting cell line repository number GM3573. Another mouse myeloma cell line that may be used is the 8-azaguanine-resistant mouse murine myeloma SP2/0 non-producer cell line.

Methods for generating hybrids of antibody-producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 proportion, though the proportion may vary from about 20:1 to about 1:1, respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. Fusion methods using Sendai virus have been described by Kohler and Milstein (1975; 1976), and those using polyethylene glycol (PEG), such as 37% (v/v) PEG, by Gefter et al. (1977). The use of electrically induced fusion methods is also appropriate (Goding pp. 71-74, 1986).

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Fusion procedures usually produce viable hybrids at low frequencies, about 1×10^{-6} to 1×10^{-8} . However, this does not pose a problem, as the viable, fused hybrids are differentiated from the parental, unfused cells (particularly the unfused myeloma cells that would normally continue to divide indefinitely) by culturing in a selective medium. The selective medium is generally one that contains an agent that blocks the *de novo* synthesis of nucleotides in the tissue culture media. Exemplary and preferred agents are aminopterin, methotrexate, and azaserine. Aminopterin and methotrexate block *de novo* synthesis of both purines and pyrimidines, whereas azaserine blocks only purine synthesis. Where aminopterin or methotrexate is used, the media is supplemented with hypoxanthine and thymidine as a source of nucleotides (HAT medium). Where azaserine is used, the media is supplemented with hypoxanthine.

The preferred selection medium is HAT. Only cells capable of operating nucleotide salvage pathways are able to survive in HAT medium. The myeloma cells are defective in key enzymes of the salvage pathway, e.g., hypoxanthine phosphoribosyl transferase (HPRT), and they cannot survive. The B cells can operate this pathway, but they have a limited life span in culture and generally die within about two weeks. Therefore, the only cells that can survive in the selective media are those hybrids formed from myeloma and B cells.

This culturing provides a population of hybridomas from which specific hybridomas are selected. Typically, selection of hybridomas is performed by culturing the cells by single-clone dilution in microtiter plates, followed by testing the individual clonal supernatants (after about two to three weeks) for the desired reactivity. The assay should be sensitive, simple and rapid, such as radioimmunoassays, enzyme immunoassays,

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cytotoxicity assays, plaque assays, dot immunobinding assays, and the like.

The selected hybridomas would then be serially
5 diluted and cloned into individual antibody-producing
cell lines, which clones can then be propagated
indefinitely to provide MABs. The cell lines may be
exploited for MAB production in two basic ways. A sample
of the hybridoma can be injected (often into the
10 peritoneal cavity) into a histocompatible animal of the
type that was used to provide the somatic and myeloma
cells for the original fusion. The injected animal
develops tumors secreting the specific monoclonal
antibody produced by the fused cell hybrid. The body
15 fluids of the animal, such as serum or ascites fluid, can
then be tapped to provide MABs in high concentration.
The individual cell lines could also be cultured *in*
vitro, where the MABs are naturally secreted into the
culture medium from which they can be readily obtained in
20 high concentrations. MABs produced by either means may
be further purified, if desired, using filtration,
centrifugation and various chromatographic methods such
as HPLC or affinity chromatography.

25 A molecular cloning approach may also be used to
generate monoclonals. For this, combinatorial
immunoglobulin phagemid libraries are prepared from RNA
isolated from the spleen of the immunized animal, and
phagemids expressing appropriate antibodies are selected
30 by panning using cells expressing the antigen and control
cells. The advantages of this approach over conventional
hybridoma techniques are that approximately 10^4 times as
many antibodies can be produced and screened in a single
round, and that new specificities are generated by H and
35 L chain combination which further increases the chance of
finding appropriate antibodies.

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The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow
5 represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many
10 changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

15

EXAMPLE I

Position Effect at *S. cerevisiae* Telomeres

Position effect is a term used to describe phenomena in which a gene's behavior is affected by its location on
20 the chromosome (Lima-de-Faria, 1983b). The change in behavior can be manifested in a variety of ways, such as a difference in phenotype, transcription level, recombination frequency, or replication timing. Although position effects have been reported in insects, plants,
25 and mice, most studies have been carried out in *Drosophila*, where euchromatic genes translocated near or within centromeric heterochromatin come under a position effect, typically exhibiting phenotypic repression (Spofford, 1976). More recently, in *S. cerevisiae* the
30 silent mating type loci, *HML* and *HMR*, have been shown to exert a position effect on the transcription of nearby genes (Brand et al., 1985; Mahoney and Broach, 1989; Schnell and Rine, 1986).

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Telomeric DNA in ciliates, humans, and probably other eukaryotes, facilitates the complete replication of linear DNA molecules by serving as substrates for

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telomerase (Zakian, 1989; Blackburn, 1990). Telomeres act as chromosome "caps"; in contrast to ends generated by chromosome breakage, telomeres are protected from exonucleolytic degradation and end-to-end fusions.

5 Telomeres are also implicated in establishing nuclear organization by engaging in associations with other telomeres and with the nuclear envelope (Agard and Sedat, 1983; Lima-de-Faria, 1983a).

10 In *S. cerevisiae*, the simple DNA repeat (TG₁₋₃) is found at the ends of all linear chromosomes (Shampay et al., 1984; Walmsley et al., 1984). The repeated sequence is necessary and sufficient in *cis* to provide telomere function *in vivo* (Wellinger and Zakian, 1989):
15 telomeric repeats are required at each end of a DNA molecule in order for it to be maintained in a linear form in yeast (Lundblad and Szostak, 1989; Pluta and Zakian, 1989). Examination of chromosomal ends reveals a heterogeneity in the number of (TG₁₋₃) repeats at
20 individual telomeres both within and between strains, with an average of ~300 bp (Shampay and Blackburn, 1988; Walmsley and Petes, 1985). In addition to the (TG₁₋₃) repeats at the ends of chromosomes, most yeast telomeres bear middle repetitive elements called telomere
25 associated sequences (Chan and Tye, 1983a; Chan and Tye, 1983b).

In *S. cerevisiae* there are two types of telomere associated sequences: Y' is a highly conserved sequence
30 that exists in a long (~6.7 kbp) and short form (5.2 kbp), whereas X is less well conserved and ranges in size from 0.3 to 3.8 kbp. The sequences can occur in tandem arrays near the ends of the chromosome, where they are separated from one another by tracts of (TG₁₋₃) 50-130 bp
35 in length (Walmsley et al., 1984). It is unclear whether the X and Y' sequences serve a particular function, since they are absent from some telomeres (Jager and

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Philippsen, 1989; Zakian and Blanton, 1988); however in humans and *Drosophila* telomere associated sequences have been implicated in meiotic chromosome pairing and the establishment of heterochromatin (Ellis et al., 1989; 5 Young et al., 1983).

In order to understand better the properties of telomeres, the inventors began an investigation to map in vivo protein-DNA interactions at chromosomal termini in 10 *S. cerevisiae*. The inventors chose to examine a single telomere by introducing a unique marker adjacent to the tract of (TG₁₋₃) DNA at the end of a chromosome. However, early in the course of such investigations it was realized that the transcription of the gene used to mark 15 the telomere was altered. In this example, the inventors demonstrate that in *S. cerevisiae*, telomeres without an X or Y' exert a position effect on the expression of genes located nearby.

20 When *URA3*, *TRP1*, *HIS3*, or *ADE2* was located near a telomere, the gene's transcription was repressed. However, the expression of each gene was reversible between states of repressed and active transcription. Both transcriptional states were inherited mitotically in 25 a semi-stable manner. Switching between the states appears to be under epigenetic control. At a locus ~20 kbp from the telomere, transcription of *URA3* was not repressed, even when an 81 bp tract of (TG₁₋₃) sequence was located adjacent to the gene. However, the internal 30 81 bp tract spontaneously became a telomere at a frequency of $\sim 10^{-6}$, and in so doing repressed the expression of the *URA3* gene. This example therefore provides genetic methods for analyzing telomere structure, and formation of new telomeres from internal 35 telomeric DNA sequences.

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A. MATERIAL & METHODS

1. Construction of Plasmids

5 Plasmid pVII-L URA3-TEL was constructed in two steps, beginning with the plasmid pYTCA-1. Plasmid pYTCA-1 has the 125 bp *Hae* III-*Mnl* I fragment from pYt103, that contains 81 bp of (TG₁₋₃) sequence derived from a yeast telomere, in the *Sma* I site of pUC9 (Runge and Zakian, 1989; Shampay et al., 1984). The (TG₁₋₃) sequence is oriented such that digestion of pYTCA-1 with *Eco* RI will yield an end that is a substrate for telomere formation in yeast. Plasmid pYTCA-1 was digested with *Hind* III and *Hinc* II and a 1.1 kbp *Hind* III-*Sma* I DNA fragment that contains the *URA3* gene was ligated between these sites (Rose et al., 1984) to form pURA3-TEL. Plasmid YA4-2 (obtained from V. Williamson) contains the *ADH4* gene on an *Eco* RI-*Bgl* II fragment inserted within the *Eco* RI-*Bam* HI sites of pUC8 (Walton et al., 1986; Williamson and Paquin, 1987). Plasmid pURA3-TEL was digested with *Hind* III and the 1.2 kbp *Hind* III fragment of pYA4-2 was ligated within, such that the *Sal* I site of the inserted fragment was positioned away from the *URA3* gene. This results in plasmid pVII-L URA3-TEL.

25 Plasmid *adh4::URA3-TEL* was also constructed in two steps. First, pVII-L URA3-TEL was digested with *Bam* HI, the DNA ends were made blunt by treatment with T4 DNA polymerase and dNTPs, and the plasmid was recircularized. Next, this new plasmid, pVII-L URA3-TEL (-*Bam* HI), was digested with *Eco* RI, the ends were made blunt as before, and ligated to the blunt-ended 1.8 kbp *Hind* III-*Eco* RI fragment of YA4-2. Plasmids with the *Bam* HI site furthest from the (TG₁₋₃) sequence have the correct orientation of the insert.

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Plasmid *adh4::URA3* was constructed by digesting
pVII-L *URA3-TEL* with *Bam* HI, making the ends blunt, then
treating the plasmid with *Eco* RI; the 1.8 kbp *Hind*
III-*Eco* RI fragment of YA4-2 with only its *Hind* III end
5 made blunt, was ligated into the plasmid.

Plasmid V-R *URA3-TEL* was made by digesting pVII-L
URA3-TEL with *Hind* III and replacing the *ADH4* derived
sequence with the 2.8 kbp *Hind* III fragment of plasmid
10 B6-10H, such that the *Eco* RI site of the insert was
furthest from the *URA3* gene. Plasmid B6-10H (obtained
from C. Newlon) contains ~19 kbp of unique DNA sequence
from the region adjacent to the subtelomeric Y' repeat on
the right arm of chromosome V (Chan and Tye, 1983b;
15 McCarroll and Fangman, 1988). The 2.8 kbp *Hind* III
fragment from B6-10H used in this study is unique
sequence ~5.5 kbp from the Y' repeat.

Plasmid pULA was constructed in a two step process.
20 First, the 1.1 kbp *Hind* III -*URA3* fragment was inserted
into the *Hind* III site of a pUC9 derivative, in which the
Pst I site has been deleted. The resulting plasmid was
digested with *Pst* I and *Nsi* I; the coding sequence of
URA3 was removed and replaced with a 4 kbp *Pst* I fragment
25 containing *LEU2* isolated from YEP13 (Broach et al.,
1979).

Plasmids pADHIS3(+), pADHIS3(-), pADADE2(+),
pADADE2(-), pADTRP1(+), and pADTRP1(-) were all
30 constructed by inserting the wild-type *HIS3*, *ADE2*, or
TRP1 genes in either orientation, into the *Bam* HI site in
the vector VII-L *URA3-TEL*. For *HIS3*: A 1.85 kbp *Bam* HI
fragment from plasmid pHIS3 (Struhl, 1985; obtained from
K. Runge) was inserted into the *Bam* HI site of
35 VII-L-*URA3-TEL*. Two plasmids are formed: pADHIS3(+), in
which the *HIS3* gene is in the same transcriptional

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orientation as the *URA3* gene, and *pADHIS3(-)* which has the *HIS3* gene in the opposite orientation.

For *ADE2*, a 3.6 kbp *Bam* HI fragment in plasmid pL909
5 (obtained from R. Keil), was inserted into the *Bam* HI
site of the vector VII-L *URA3*-TEL. The resulting plasmids
were designated *pADADE2(+)*, indicating *ADE2* transcription
in the same direction as the adjacent *URA3* gene, or
pADADE2(-) for *ADE2* transcription in the opposite
10 direction.

For *TRP1*, 0.85 kbp *Eco* RI-*Bgl* II fragment from
plasmid YRp7 (Struhl et al., 1979) was blunt-ended with
T4 DNA polymerase and inserted into the *Bam* HI site in
15 VII-L *URA3*-TEL which also had the *Bam* HI ends filled-in
with T4 DNA polymerase. The plasmid with the *TRP1* gene
in the same transcriptional orientation as *URA3* was
denoted *pADTRP1(+)*, while the plasmid in which *TRP1*
transcription was in the opposite direction as *URA3*
20 transcription was *pADTRP1(-)*.

Plasmid *TRP1*/RS306 was made by inserting the *Eco*
RI-*Bgl* II fragment of *TRP1* into the *Eco* RI-*Bam* HI site of
pRS306 (Sikorski and Hieter, 1989).
25

E. coli strain MC1066 (*r⁻ m⁻*, *trpC9830*, *leuB600*,
pyrF::Tn5, *lacΔX74*, *strA*, *galU*, *galK*) was used as a host
for all plasmids (Casadaban et al., 1983). LB medium
with ampicillin (100 μg/ml) and M9 medium supplemented
30 with appropriate amino acids were prepared as described
by Maniatis et al. (Maniatis et al., 1982).
Complementation of MC1066 mutations by the homologous
yeast genes was used when applicable.

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2. Yeast Strains & Methods

Media used for the growth of *S. cerevisiae* were based on synthetic complete media as described by Sherman et al. (Sherman et al., 1986) to which uracil (35 mg/l), tyrosine and lysine (60 mg/l), and leucine and isoleucine (80 mg/l) had been added. One gram of 5-FOA per liter of media was added to determine resistance to 5-FOA. Medium for ADE2 red/white sector colony growth was as described (Klapholz and Esposito, 1982) except arginine was 50 mg/l and threonine was 100 mg/l. Colonies were grown for three days at 30°, then incubated for 1-2 weeks at 4° for full color development. *S. cerevisiae* transformation was performed using the lithium acetate procedure (Ito et al., 1983).

To delete the *URA3* gene, strain 1GA2 (*MAT α ade2 ade5 leu2-3,112 lys5 cyh2^r can1^r*; made in this study) was transformed with *Hind* III digested pULA (see above), and Leu⁺ colonies were isolated. The structure of the chromosome from which *URA3* was deleted was checked by Southern analysis in Leu⁺ isolates that also tested Ura⁻. DG20 is the *ura3 Δ ::LEU2* derivative of 1GA2. Strains DG26, DG27, DG28, and DG30 were constructed by transforming DG20 with different DNA fragments: DG26 with plasmid *adh4::URA3-TEL* cleaved by *Bam* HI and *Sal* I, DG27 with plasmid *adh4::URA3* cleaved by *Bam* HI and *Sal* I, DG28 with plasmid VII-L *URA3-TEL* cleaved by *Sal* I and *Eco* RI, and DG30 with plasmid V-R *URA3-TEL* cleaved by *Eco* RI. All transformants were selected as being both Ura⁺ and Leu⁺. The expected structure for each transformant was verified by Southern analysis. In each case, total genomic DNA was cleaved twice, once by *Bgl* II and once by *Pst* I. The Southern blots of DG26, DG27, and DG28 were hybridized with a series of DNA probes which included: the 1.1 kbp *Hind* III *URA3* gene, the proximal *ADH4* probe, and the distal *ADH4* probe. The structure of DG30 was

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verified in a similar manner using probes from plasmid B6-10H.

Strains UCC41, UCC42, UCC45, UCC61, UCC62, UCC63,
5 UCC81, UCC82, and UCC83 were derived from strain 4-1
(*MAT α lys2 his4 trp1 Δ ade2 leu2-3,112 ura3-52* made in
this study), by transforming strain 4-1 with different
DNA fragments and selecting for Ura⁺ colonies: UCC41 with
10 pADADE2(+) cut with *Sal* I and *Not* I, UCC42 with
pADADE2(-) cut with *Sal* I and *Not* I, UCC45 with pL909 cut
with *Bam* HI, UCC61 by pADTRP1(+) cut with *Sal* I and *Eco* RI,
UCC62 with pADTRP1(-) cut with *Sal* I and *Eco* RI,
UCC81 with VII-L URA3-TEL cut with *Sal* I and *Eco* RI,
UCC82 with *adh4::URA3* cut with *Bam* HI and *Sal* I, UCC83
15 with pUCU (contains the 1.1 kbp *Hind* III fragment
containing the *URA3* gene in pUC9) cut with *Hind* III, and
UCC63 with pTRP1/RS306 digested with *Nde* I.

Strains UCC51, UCC52, UCC53, UCC74, UCC75, and UCC76
20 were derived from strain 3482-16-2 (*MAT α , met2, his3D-1,*
leu2-3,112, trp1-289, ura3-52, obtained from L.
Hartwell), by transforming strain 3482-16-2 with
different DNA fragments, again selecting for Ura⁺
colonies: UCC51 by pADHIS3(+) cut with *Sal* I and *Eco* RI,
25 UCC52 with pADHIS3(-) cut with *Sal* I and *Eco* RI, UCC53
with pHIS3 cut with *Bam* HI, UCC74 with VII-L URA3-TEL cut
with *Sal* I and *Eco* RI, UCC75 with *adh4::URA3* cut with *Bam*
HI and *Sal* I, and UCC76 with pUCU cut with *Hind* III. The
expected chromosome structure of each transformant was
30 verified by Southern analysis.

3. Selection for 5-FOA^R Colonies

Cells were grown into colonies for 2-3 days at 30°
35 on YC plates or plates that lacked uracil. Colonies were
picked and resuspended in 1.0 ml H₂O, serial dilutions
were made and an appropriate amount of cell suspension

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was spread to produce ~200 colonies/plate. Cells were spread onto 5-FOA^R plates for selection, and YEPD, YC, or synthetic complete media plates to determine the total number of colony forming cells. The number of colonies on a plate was determined after 3-4 days of growth at 30°.

4. Analysis of Nucleic Acids from *S. cerevisiae*

S. cerevisiae cells were grown in 5 ml of YEPD to stationary phase, and total genomic DNA was isolated by disrupting cells with glass beads as described (Runge and Zakian, 1989). Methods for cleavage of total genomic DNA with restriction enzymes, gel electrophoresis, and Southern hybridizations have been previously described (Gottschling and Cech, 1984; Runge and Zakian, 1989). For rehybridization studies, probes were removed from blots with boiling water.

Cells were grown to a density of $0.5-2 \times 10^7$ cells/ml and total RNA was isolated as described (Sherman et al., 1986), except that the nucleic acids were precipitated with 2 vol. ethanol and resuspended in water at a concentration of 1-10 mg/ml. RNA concentration was determined by UV spectroscopy. Ten or twenty μg of total RNA was separated by electrophoresis on a 1.5% agarose-formaldehyde-MOPS gel and transferred to nitrocellulose or nylon membrane as described (Ogden and Adams, 1987; Wahl et al., 1987). Strand specific RNA probes were made by in vitro transcription of linearized plasmids with T7 polymerase in the presence of [α -³²P] CTP (~600 Ci/mmol) (Wahl et al., 1987).

Plasmids used for transcription were derivatives of pVZ1 (Eghtedarzadeh and Henikoff, 1986); the *URA3* probe contained the *Pst* I-*Nco* I fragment of the gene, the *HIS3* probe contained the *Bam* HI-*Kpn* I fragment of the gene,

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the *TRP1* probe contained the *Hind* III-*Bgl* II fragment of the gene. Northern hybridization was performed as described (Wahl et al., 1987). Multiple exposures of autoradiograms were scanned with an LKB Ultrosan XL
5 densitometer to determine the relative levels of *URA3* or *HIS3* mRNA.

B. RESULTS

10 1. Marking a Telomere with *URA3*

URA3, which is required for uracil biosynthesis, is normally found near the centromere on chromosome V. The entire gene, including the *cis* elements required for its
15 normal regulation, is located on a 1.1 kbp *Hind* III-*Sma* I fragment (Rose et al., 1984). This fragment was used in all of the *URA3* constructs described in this example. Studies were carried out in haploid yeast strains that contained either of two non-reverting *ura3*⁻ alleles:
20 *ura3-52*, which contains a Ty transposon insertion within the *URA3* coding sequence (Rose and Winston, 1984) (UCC series), or *ura3Δ::LEU2*, in which the entire coding region of *URA3* on chromosome V has been replaced by the *LEU2* gene (DG series).

25 *ADH4* is the most distal gene on the left arm of chromosome VII (Walton et al., 1986). Fragment mediated transformation (Rothstein, 1983) was used to introduce *URA3* onto the left arm of chromosome VII, to create the
30 haploid strain DG28. In DG28, a portion of *ADH4* and the DNA distal to it are deleted and replaced with *URA3* and an 81 bp stretch of (TG₁₋₃). After transformation into yeast, the 81 bp are extended to ~300 bp of (TG₁₋₃), a length typical of all other telomeres in this strain.
35 Transcription of the *URA3* gene is towards the telomere, with its promoter ~1.3 kbp from the end of the chromosome.

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2. Position Effect at Yeast Telomeres

The chemical 5-fluoro-orotic acid (5-FOA) can be used in the negative selection of *URA3* expression; 5-FOA is converted into a toxic substance by the *URA3* gene product (Boeke et al., 1987). The constitutive level of *URA3* expression in a cell is normally sufficient to yield cells sensitive to 5-FOA (5-FOA^S). Resistance to 5-FOA (5-FOA^R) can be used as a method to select for cells that have lost or mutated the wild type *URA3* gene. Therefore, sensitivity to 5-FOA was used as a means to determine *URA3* expression as a function of chromosomal location.

The frequency of a spontaneous 5-FOA^R allele arising at the normal *URA3* locus is $\sim 10^{-7}$ (1GA2; Boeke et al., 1984). Since 5-FOA^R cells derived in this way have mutations in the *URA3* gene, they are Ura⁻ (i.e. unable to grow in the absence of uracil). In contrast, when cells with *URA3* at the telomere (DG28) were pre-grown in media containing uracil (no selection for *URA3* expression) and then plated for single colonies onto 5-FOA, 33% of the cells gave rise to 5-FOA^R colonies (DG28). Moreover, when these 5-FOA^R colonies were replica-plated to media that lacked uracil, cells were able to grow. That is, the cells were still *URA3*⁺. These results suggested that the 5-FOA^R exhibited by these cells was not due to an inordinately high mutation rate in or loss of the *URA3* gene, but rather that *URA3* expression at the telomere was reduced below the killing threshold of 5-FOA. Nonetheless, cells in an 5-FOA^R colony still had the ability to produce sufficient *URA3* gene product to overcome a lack of uracil in the medium.

When DG28 cells were pre-grown in medium lacking uracil (selecting for *URA3* expression), one out of 10^5 cells produced a colony on plates containing 5-FOA. Once again, each of these 5-FOA^R colonies was still *URA3*⁺.

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Taken together these results suggested that under non-selective growth conditions expression of the *URA3* gene in about one-third of the DG28 cells was sufficiently repressed to allow growth on 5-FOA, but that under
5 selection, expression of the telomere-linked *URA3* gene is still possible in many or all of the cells. The resistance to 5-FOA of cells with *URA3* at the VII-L telomere has been observed in a number of strains. While there have been strain specific differences in the
10 fraction of 5-FOA^R cells when cells were pre-grown under non-selective conditions, these values (0.10-0.90) were all within an order of magnitude of one another (UCC74 & UCC81), and indicate that repression of a telomere-linked *URA3* gene on VII-L is a general phenomenon.

15

This unexpected behavior of the *URA3* phenotype (colonies that were 5-FOA^R yet still Ura⁺) caused the inventors to examine the steady state levels of *URA3* mRNA in cells with the gene either at its normal chromosomal
20 position or at the telomere of VII-L. RNA was isolated from cells grown under either selective or non-selective conditions for *URA3* expression. Consistent with earlier studies, cells with *URA3* at its normal chromosomal locus had a modest increase in *URA3* mRNA levels (~1.4-fold)
25 when grown under selective conditions compared to growth under non-selective conditions (strain 1GA2) (Bach et al., 1979; Lacroute, 1968; Rose and Botstein, 1983). However, a major difference in *URA3* mRNA levels was observed in cells with the *URA3* gene at the telomere.
30 RNA levels in DG28 cells grown under non-selective conditions were one-fifth that of cells with *URA3* at its normal locus (DG28 & 1GA2).

In contrast, under selective conditions, RNA levels
35 in cells with *URA3* at the telomere were equivalent to the level in cells with *URA3* at its normal locus (strains DG28 & 1GA2, INDUC). Thus consistent with the 5-FOA^R

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phenotype, the constitutive level of *URA3* RNA is significantly reduced when the gene is located next to the telomere at VII-L compared to when it is at its normal chromosomal locus. Yet under selection, the level of *URA3* RNA at the telomeric locus in DG28 cells is virtually the same as when *URA3* is at its normal chromosomal locus.

In order to determine whether repression occurs at telomeres other than VII-L, strain DG33 was constructed. This strain has the *URA3* gene inserted near the telomere on the right arm of chromosome V (V-R), in a manner similar to that for *URA3* on VII-L in strain DG28. Determination of the fraction of 5-FOA^R colonies and analysis of mRNA levels in strain DG33 indicates that constitutive expression of *URA3* is also repressed at this telomere. The difference in the fraction of 5-FOA^R cells between the two strains (0.33 for DG28, 0.04 for DG33) presumably reflects differences between individual telomeres in terms of their specific chromosomal environments.

URA3 was also repressed when positioned near the telomere of a telocentric version of chromosome IV or of a 60 kbp artificial linear chromosome. Thus the ability to repress the expression of a nearby *URA3* gene appears to be a general property of *S. cerevisiae* telomeres.

3. Repression by Proximity to Telomeres Occurs for Other Genes

In general, a region of the chromosome that exerts a position effect does so in a gene non-specific manner. Therefore the inventors examined whether genes other than *URA3* were repressed by proximity to a telomere. The *TRP1*, *HIS3*, or *ADE2* gene was inserted between *URA3* and the telomere DNA sequence at the *Bam* HI site of plasmid

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'VII-L URA3-TEL'. Each gene was inserted in both orientations. These constructs were then used to introduce *TRP1*, *HIS3*, or *ADE2* adjacent to the VII-L telomere, by selecting for *URA3* expression. In selecting
5 only for *URA3* expression during strain construction, no selective pressure was placed upon the telomeric *TRP1*, *HIS3*, or *ADE2* genes.

10 In strains bearing a telomere-linked copy of *TRP1*, and grown under non-selective conditions, *TRP1* RNA was undetectable by Northern analysis, regardless of the gene's orientation at the telomere (UCC61 & UCC62). By examining very long exposures of the autoradiograms the inventors estimated that the RNA level from the telomeric
15 *TRP1* was $\leq 1\%$ of the RNA level when the same *TRP1* fragment was located at an internal chromosomal site within the normal *URA3* locus on chromosome V.

20 Colonies of cells with *TRP1* at the telomere or at an internal locus were grown on non-selective medium and then plated in serial dilution to medium that lacked tryptophan. All of the cells with *TRP1* at an internal site on the chromosome (UCC63) formed colonies on plates lacking tryptophan. However, those with *TRP1* at the
25 telomere showed a reduction in colony forming ability on plates lacking tryptophan (UCC61 & UCC62). Only 10^{-2} cells with *TRP1* oriented such that transcription was directed towards the telomere formed colonies in the absence of tryptophan (UCC61). When *TRP1* transcription
30 was away from the telomere, $\sim 10^{-3}$ cells formed colonies (UCC62). In addition, the UCC61 cells formed robust colonies in three days, while the UCC62 colonies were smaller.

35 The telomeric *TRP1* RNA levels and plating efficiency data indicate that under non-selective growth conditions the majority of cells with *TRP1* near the telomere had

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very low or no *TRP1* expression. In all three *TRP1* constructs described, a portion of the UAS/promoter elements found at the normal *TRP1* locus was missing (Kim et al., 1986). While these missing elements have no
5 apparent effect on the ability of cells to grow without tryptophan when *TRP1* is at an internal locus, their absence may explain why *TRP1* expression was more severely repressed at the telomere compared to the expression of *URA3* at the telomere.

10

When *HIS3* was placed at the telomere and its transcription was directed away from the telomere, there was a detectable reduction in RNA levels compared to when the gene was at its normal chromosomal locus (UCC52).

15

When the direction of transcription at the telomere was reversed, there was a slight increase in RNA levels (UCC51). Phenotypically, there was a modest (less than ten-fold) reduction in plating efficiency on media lacking histidine for UCC52, but no effect on UCC51, a
20 result consistent with the relative RNA levels.

4. Transcriptional Repression at Telomeres is Reversible and Inherited in a Semi-Stable Fashion

25

As shown above, when the *URA3* gene was telomere-linked (DG28), cells from colonies that were 5-FOA^R could still grow when placed on medium lacking uracil.

Conversely, cells grown in the absence of uracil were
30 able to form colonies when placed on medium containing 5-FOA. These results suggested that a telomere-linked *URA3* gene could switch between repressed and active transcriptional states. The *ADE2* gene provides a convenient color assay for determining whether the gene
35 is expressed; *ADE2*⁺ colonies are white, whereas *ade2*⁻ colonies are red (Roman, 1956). Thus, expression of a telomere-linked *ADE2* gene can be monitored by determining

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the color of colonies produced by cells carrying this marked telomere.

When the *ADE2* gene was placed at the telomere such
5 that *ADE2* transcription was directed towards the telomere
(UCC41), all colonies contained red and white sectors.
This sectorized phenotype indicated a switch between the
repressed and active transcriptional states of *ADE2*
during colony development. The colonies displayed a wide
10 range of sectoring phenotypes. Some colonies were
primarily white (active) and gave rise to red (repressed)
sectors near the periphery. An equal number of colonies
were primarily red with white sectors near the periphery.
Intermediate levels of sectoring between these two
15 extremes were also readily visible.

In some colonies multiple switches between
transcriptional states can be inferred. For example, a
predominantly red colony has a large white sector.
20 Within this white portion, red sectors are clearly
visible. The reversibility was further demonstrated by
isolating cells within a white (or red) sector and
plating them for single colonies. Each new colony
contained red and white sectors. In contrast with the
25 results in UCC41, when *ADE2* transcription was directed
away from the telomere (UCC42), no red sectors were
observed in a colony.

These results demonstrate that the expression of a
30 telomere-linked *ADE2* gene can switch between an active
and repressed state, and that the expression state is
semi-stable during mitotic growth. Based on the results
with *URA3*, *TRP1*, and *HIS3*, the inventors infer that the
control of *ADE2* expression is at the transcriptional
35 level. However, it was not possible to determine the
level of RNA produced at the telomere-linked *ADE2*,

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because an identical sized transcript was made by the *ade2* allele at its normal chromosomal locus.

The probability of a telomere-linked *ADE2* gene
5 (UCC41) being in an active (repressed) transcriptional
state was estimated from the fraction of predominantly
white (red) colonies. Five colonies of UCC41 cells grown
on non-selective medium, were plated for single colonies
10 onto non-selective medium. Approximately equal numbers
of colonies were found that had primarily red centers
giving rise to white sectors, and primarily white centers
that gave rise to red sectors. This result indicates
that a telomere-linked *ADE2* gene on VII-L has an about
equal probability of being in an active or repressed
15 transcriptional state.

However, when five colonies of UCC41 were pre-grown
in the absence of adenine (selecting for *ADE2* expression)
and then plated onto non-selective plates, there were up
20 to nine times as many colonies with white centers than
with red centers. Closer examination of colonies with
white centers revealed that red sectors generally did not
appear until very close to the periphery of the colony.
This observation suggested that the active expression
25 state of *ADE2* was stable for many generations. The
distance from the center of these colonies to the points
at which multiple red sectors appeared was measured.
This value was used to compute the fraction of the total
colony volume (assuming a half sphere geometry for a
30 colony) that comprised the non-sectored center of the
colony. The number of cells within this region of the
colony was calculated (assuming there are $\sim 10^8$ cells in a
colony), and this value was used to derive the number of
cell divisions required to produce the quantity of white
35 cells from a single progenitor. From these calculations
the inventors estimate that the active transcriptional

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state of *ADE2* is inherited for 15-20 generations in these colonies.

The phenotypic switching displayed by *ADE2* at a telomere was also observed with the *URA3* gene using a single cell analysis. Freshly budded cells grown on medium containing 5-FOA were moved by micromanipulation to a region of the plate where they could develop into full colonies. The majority (81/119) of the cells formed colonies, but 8% (9/119) of the cells formed microcolonies consisting of 4-8 cells. Microcolonies were not detected in a control study in which no 5-FOA was present in the medium. Therefore the microcolonies presumably represent cells arrested in growth on the 5-FOA due to the *URA3* gene being switched to an actively expressing state after budding. The cells that did not form colonies may have been progeny of cells that had switched to an actively expressing state prior to budding, or were inviable as a result of the micromanipulation method. A rough value for the switching of *URA3* from a repressed to an active state in DG28 cells was calculated by dividing the number of cells that formed microcolonies (9) by the total number of colony forming cells (9+81), which yields an estimated switch rate of 10^{-1} per division.

5. The Distance Over which Telomeres Exert a Position Effect on *URA3* Expression

In order to obtain an estimate of the distance over which the telomere exerted a position effect, the *URA3* gene was placed ~20 kbp from the end of the left arm of chromosome VII by insertion within the *ADH4* locus (DG27). Based on both RNA analysis and the frequency of 5-FOA^R colony formation, cells with *URA3* inserted within *ADH4* had levels of *URA3* expression comparable to cells with *URA3* at its normal locus, under either selective or

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non-selective growth conditions. Thus on the left arm of chromosome VII the telomeric repression was no longer detectable when *URA3* was ~20 kbp from the telomere.

5 In order to determine whether repression occurred over distances less than 20 kbp from the telomere, the constructs described above, in which *TRP1*, *HIS3*, or *ADE2* was inserted between *URA3* and the telomere DNA sequence, were analyzed for *URA3* expression. The inserted genes
10 increased the distance between *URA3* and the telomere by 0.85, 1.8, or 3.6 kbp, respectively.

 Cells with each of the constructs were pre-grown in complete synthetic medium, thus no selection for the
15 expression of *URA3* or the inserted gene was introduced. The cells were then plated to medium containing 5-FOA and the fraction of 5-FOA^R colonies was determined. The analysis revealed that as the distance between *URA3* and the telomere was increased, the level of repression
20 decreased. For instance, insertion of the 0.85 kbp *TRP1* fragment yielded 5-FOA^R colonies at a frequency of 0.02-0.14 (UCC61 and UCC62), while insertion of the 3.6 kbp *ADE2* fragment yielded $\leq 10^{-5}$ 5-FOA^R cells (UCC41 and UCC42). However, the level of *URA3* expression was also
25 influenced by the orientation of the inserted DNA fragment.

 This conclusion was best demonstrated by the result with the *HIS3* fragment: when transcription of the *HIS3*
30 gene was towards the telomere (UCC51), $\sim 10^{-4}$ cells were 5-FOA^R; when *HIS3* transcription was away from the telomere (UCC52), 0.26 of the cells were 5-FOA^R. The orientation of *TRP1* and *ADE2* had smaller, but detectable effects on *URA3* expression. Thus further studies on the level of
35 *URA3* expression as a function of distance from the telomere must take into account both the composition and

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orientation of the DNA sequences located between the telomere and *URA3*.

5 **6. Internal Tracts of (TG₁₋₃) Do Not Cause
 Repression, but they Can Become Chromosome Ends
 and Consequently Cause Position Effect**

 Internal tracts of (TG₁₋₃) sequence occur naturally
 between the telomere associated elements X and Y' and
10 between tandem Y' elements (Chan and Tye, 1983a; Chan and
 Tye, 1983b). Internal (TG₁₋₃) tracts range from 50 to 130
 bp in length (Walmsley et al., 1984). In order to
 determine whether these internal (TG₁₋₃) sequences might
 also exert a position effect, 81 bp of (TG₁₋₃) were
15 introduced adjacent to the telomeric side of *URA3*, within
 the *ADH4* locus (DG26).

 RNA levels in these cells were somewhat higher than
 in cells with *URA3* at its normal locus or at the *ADH4*
20 locus without (TG₁₋₃) (DG26, DG27, & 1GA2). This elevated
 transcription was true for both constitutive and induced
 URA3 gene expression. These elevated mRNA levels are
 probably explained by an enhancer-like activity
 associated with (TG₁₋₃) repeat sequences when they are
25 adjacent to a gene in a non-telomeric location (Runge and
 Zakian, 1990). Whatever the mechanism responsible for
 elevated expression, the internal tract of 81 bp of (TG₁₋₃)
 at the *ADH4* locus clearly does not cause repression of
 constitutive expression. These data demonstrate that
30 (TG₁₋₃) sequences are not sufficient to cause position
 effect: the *URA3* gene must be positioned near a telomere
 (or alternatively, near a (TG₁₋₃) tract >81 bp) in order
 for transcription to be repressed.

35 Consistent with the high level of *URA3* expression
 seen in the RNA analysis, the fraction of 5-FOA^R colonies
 from cells with *URA3* next to the internal tract of (TG₁₋₃)

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and grown in uracil was $\sim 10^{-6}$ (DG26 CONST). Although this value was low compared to cells with a telomere-linked copy of *URA3*, it is an order of magnitude greater than the fraction of 5-FOA^R colonies in cells with *URA3* at its normal locus (strains 1GA2 & DG26). Replica-plating of the 5-FOA^R colonies derived from DG26 cells revealed that they were all still Ura⁺ (in contrast to 5-FOA^R colonies arising from cells with *URA3* at its normal locus, which were typically Ura⁻). This phenotype is identical to that seen for the cells with *URA3* at the telomere (i.e. DG28), suggesting that the internal (TG₁₋₃) sequences might have become telomeric in those cells able to form colonies on 5-FOA.

This hypothesis was confirmed by Southern analysis. In four out of four independent isolates in which DG26 cells gave rise to 5-FOA^R colonies, the *URA3* sequences were on a restriction fragment of the size expected for a telomeric location. In addition, Southern hybridization demonstrated that sequences immediately distal to the internal (TG₁₋₃) tract were no longer detectable in the 5-FOA^R cells. These results show that internal tracts of (TG₁₋₃) sequence can spontaneously become chromosomal ends by a mechanism that results in the deletion of sequences distal to the internal (TG₁₋₃) tract. In addition, the results provide independent evidence that the repressed expression of *URA3* at the telomere is neither an artifact of transformation, nor a mutation within the *URA3* gene or one of its trans activating factors.

C. DISCUSSION

1. Position Effect at Yeast Telomeres

A position effect was demonstrated at the telomeres of *S. cerevisiae* chromosomes. The effect resulted in reduced gene expression of telomere-linked genes as

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assayed both by amount of stable mRNA and by phenotype. For instance, cells with a telomere-linked *URA3* gene were able to grow in the presence of 5-FOA, behavior consistent with a *ura3⁻* phenotype. When *ADE2* was
5 telomere-linked many cells produced predominantly red colonies as is characteristic of *ade2⁻* cells. The position effect altered the expression of four out of four Pol II genes: *ADE2*, *HIS3*, *TRP1*, and *URA3*. In
10 addition the effect was observed at four out of four telomeres, including an artificial linear chromosome. Therefore, it can be concluded that the position effect is a general phenomenon of *S. cerevisiae* telomeres.

The position effect acted upon the *URA3* promoter at
15 distances of at least ~4.9 kbp from the telomere, but at ~20 kbp from the left end of chromosome VII the effect was not observed. In addition the influence of distance on position effect strongly depended upon the specific
DNA sequences located between *URA3* and the telomere and
20 probably other factors that are not yet well understood. For example, the transcriptional activity of *ADE2*, *HIS3*, and *URA3* was dependent upon the gene's orientation with respect to the telomere. In the process of generating
artificially fragmented linear chromosomes, Hegemann
25 et al. report a "leaky" 5-FOA^R phenotype for a *URA3* gene located 6-8 kbp from the telomere (Hegemann et al., 1988). In these constructs, most of the 6-8 kbp was the subtelomeric middle repetitive element Y'. The inventors postulate that the reported "leaky" phenotype is due to a
30 telomeric position effect and suggest that telomeric repression can act at a distance of at least 6 kbp, and through a Y' element.

The telomeric position effect appears to be a result
35 of proximity to the end of the chromosome and not simply due to the telomeric DNA sequence (TG₁₋₃). Eighty-one base pairs of (TG₁₋₃) sequence ~20 kbp from the telomere

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did not repress *URA3* expression. While longer lengths of (TG₁₋₃) were not tested at internal loci, one of several strains that were tested for telomeric position effect contained the *tell* mutation. In the *tell* strain, the
5 telomere adjacent to *URA3* had a (TG₁₋₃) tract of 95-120 bp, yet the level of 5-FOA^R in this strain was similar to that for all other strains tested. Taken together these results argue that the telomere itself, not simply (TG₁₋₃) repeats are responsible for telomeric position effect in
10 *S. cerevisiae*.

The repressed state conferred by the telomere was mitotically inherited over a number of generations, but the genes could escape from repression and switch to a
15 state of active transcription. This reversibility was visually demonstrated by the red and white sectorized colonies of cells with *ADE2* near the telomere (UCC41), and was also supported by the single cell analysis of DG28 cells on 5-FOA. The transcriptional state of a
20 gene, whether repressed or active, appeared to be stable over many generations.

The switching between active and repressed transcriptional states for genes at telomeres is not due
25 to genetic alteration, but rather to an epigenetic switch. Several lines of evidence support this interpretation: 1. The repression was readily reversible, in the presence or absence of selection. 2. There were no differences in DNA structure or copy number
30 of the telomeric genes, as judged by Southern analysis, regardless of whether these haploid cells were grown under conditions that were non-selective, or that selected for expression or repression of the genes. 3. The telomeric position effect was gene non-specific.

35

Epigenetic variation of gene expression has been observed in plants, insects, mammals, and *S. cerevisiae*.

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In *Drosophila*, position effect variegation is observed when a euchromatic gene is moved within or near a heterochromatic region of the chromosome (Eissenberg, 1989; Spofford, 1976). Heterochromatin is a portion of the chromosome which remains visibly condensed throughout interphase of the cell cycle. In contrast, euchromatin decondenses after telophase and appears diffuse during interphase. When the *white* gene is located near some types of heterochromatin, a 'salt-and-pepper' mosaicism in eye color is observed (Spofford, 1976). This mosaicism is visually analogous to the sectorized colonies produced by cells with *ADE2* at the telomere, and it could be inferred that similar mechanisms are at work in the two organisms.

In *S. cerevisiae*, epigenetic switching has been reported at the silent mating type locus, *HML* (Pillus and Rine, 1989). In a wild type cell *HML α* is not expressed. However in a *sir1* strain, *HML α* switches between repressed and expressed states. Current models for the *HML* switch favor a change in chromatin conformation between the two phenotypic states. Besides changes in chromatin structure, postulated mechanisms of epigenetic variation in plants and mammals include changes in DNA methylation, topology, and nuclear locale (Fedoroff et al., 1989; Holliday, 1987; Monk, 1990; Weintraub, 1985).

Cytological observations in plants, insects, and mammals indicate that telomeres occupy specific regions within the nucleus and are frequently associated with the nuclear envelope (Lima-de-Faria, 1983a; White, 1973). In addition, telomeres are usually packaged as heterochromatin (Fussell, 1975; Traverse and Pardue, 1989). In the single-celled eukaryotes, *Oxytricha*, *Dictyostelium*, and *Tetrahymena*, the DNA adjacent to the chromosome termini are packaged in an orderly array of phased nucleosomes, which is consistent with the presence

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of a highly ordered chromatin structure (Budarf and Blackburn, 1986; Edwards and Firtel, 1984; Gottschling and Cech, 1984). In *Drosophila*, P element-mediated transposition of the *white* gene near the 3R telomere
5 results in mosaic expression of the gene, indicative of a position effect caused by proximity to the heterochromatin observed at this telomere (Hazelrigg et al., 1984; James et al., 1989; Levis et al., 1985).

10 It is noted that *S. cerevisiae* telomeres have two of the classic features of heterochromatin: telomeres replicate late in S phase (McCarroll and Fangman, 1988), and as shown here, they exert position effect on the expression of nearby genes. The inventors propose that
15 the phenotypic switching of telomere-linked genes in yeast is the result of a competition between the formation of a stable active transcriptional complex and the normal telomeric chromatin structure that prevents gene expression. Such a chromatin structure must
20 originate from the end of the chromosome. In *Oxytricha* the molecular ends of macronuclear mini-chromosomes are recognized by a heterodimeric protein complex (Gottschling and Zakian, 1986; Price and Cech, 1989). Similar proteins in yeast may form a telomeric structure
25 that is important in establishing the position effect.

The semi-stable, reversible repression (or expression) at yeast telomeres may be analogous to a primitive developmental switch. When cells with a
30 telomere-linked copy of *ADE2* were pre-grown under selection for *ADE2* expression, most (~80%) subsequently gave rise to colonies of primarily white (transcriptionally active) cells under non-selective growth conditions. The active transcriptional state of
35 *ADE2* can be inherited for at least 15-20 generations after removal of selection. This primitive control mechanism for gene expression may be exploited by some

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organisms to allow developmentally controlled expression of telomere-linked genes. In *Trypanosomes*, telomeres are the exclusive genomic expression sites for surface antigen genes (reviewed in (Pays and Steinert, 1988)).

- 5 Many telomeres within a cell can carry transcriptionally competent genes, yet only one such gene is expressed at a time. Perhaps the other telomere-linked genes are kept repressed, albeit reversibly, by telomeric position effect.

10

2. New Telomere Formation

- The inventors found that internal tracts of (TG₁₋₃) sequence can spontaneously become chromosomal ends.
- 15 Since the DNA distal to the (TG₁₋₃) tract is deleted, it seems unlikely that telomere formation occurred by reciprocal recombination between the internal (TG₁₋₃) sequence and another telomere. New telomere formation may have occurred through intrachromosomal recombination
- 20 between the internal (TG₁₋₃) sequence and the telomere with a resulting deletion of intervening sequences (as has been postulated for deletion of the subtelomeric repeat Y' (Horowitz and Haber, 1985)), by unequal sister chromatid exchange or conversion, or by a distal
- 25 chromosome break followed by telomere "healing" at the (TG₁₋₃) sequence.

- New telomere formation in conjunction with deletion of all terminal sequences has been observed
- 30 cytologically, and has been an area of intense interest because of its implications for chromosome breakage at fragile sites and for the generation of chromosomal abnormalities in cancer cells (Le Beau, 1988; Sutherland and Hecht, 1985). Recently it has been postulated that a
- 35 subclass of such sites might in fact be regions of the chromosome which contain internal stretches of telomeric DNA sequences (Hastie and Allshire, 1989). In this

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example the inventors find that internal tracts of telomeric DNA do indeed spontaneously become chromosomal termini, albeit at a low frequency ($\sim 10^{-6}$).

5

EXAMPLE II

Modifiers of Position Effect are Shared Between Telomeric and Silent Mating-Type Loci in *S. cerevisiae*

10 The inventors have shown that Pol II-transcribed genes succumb to a position effect when placed near the ends of chromosomes in *S. cerevisiae* (Gottschling et al., 1990; Example I), reflecting observations made in other eukaryotes that the chromosomal location of a gene can affect its expression (Eissenberg, 1989; Henikoff, 15 1990; Lima-de-Faria, 1983; Spofford, 1976; Spradling and Karpen, 1990; Wilson et al., 1990). The position effect is manifested as the stable but reversible transcriptional repression of each gene examined.

20 The mechanism by which this repression occurs is unclear, but it is likely due to a structural attribute of *S. cerevisiae* telomeres. Cytological observations in plants, insects, and mammals indicate that telomeres are heterochromatic; in addition, the telomeres in these 25 organisms and in *Trypanosomes* occupy unique locations within the nucleus, typically being associated with the nuclear envelope (Chung et al., 1990; Fussell, 1975; Hochstrasser et al., 1986; Lima-de-Faria, 1983; Rawlins and Shaw, 1990; Traverse and Pardue, 1989; White, 1973).

30

HML and *HMR* are two other loci in *S. cerevisiae* where a position effect on transcription has been observed (Klar et al., 1981; Nasmyth et al., 1981). The mating-type genes, which are expressed when present at 35 the *MAT* locus, are maintained transcriptionally silent when present at *HML* and *HMR* even though all *cis*-acting sequences required for full expression at *MAT* are

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present. Other Pol II- or Pol III-transcribed genes are also repressed when inserted within or near the *HM* loci (Brand et al., 1985; Mahoney and Broach, 1989; Schnell and Rine, 1986).

5

DNA sequences known as 'silencers' flank both *HM* loci and are required for transcriptional repression (Abraham et al., 1984; Brand et al., 1985; Feldman et al., 1984; Mahoney and Broach, 1989). The silencers (denoted "E" and "I") have been genetically dissected into smaller functional elements, which are recognition sites for DNA binding proteins; these include an ARS (Autonomous Replicating Sequence) element, and ABF1 and RAP1 binding sites (Brand et al., 1987; Buchman et al., 1988; Mahoney and Broach, 1989; Mahoney et al., 1991; Shore and Nasmyth, 1987; Shore et al., 1987). The RAP1 protein also binds to the yeast telomeric sequence (TG₁₋₃)_n (Buchman et al., 1988; Longtine et al., 1989). RAP1 is apparently involved in repression of *HM*, since *HMR* is derepressed when RAP1 temperature sensitive mutant cells are shifted to the nonpermissive temperature (Kurtz and Shore, 1991).

At least seven additional genetic loci play a role in *HM* silencing. The products of four genes, *SIR1*, *SIR2* (*MAR1*), *SIR3* (*MAR2*, *CMT*), and *SIR4* (Silent Information Regulator), are required for complete silencing at both the *HM* loci (Haber and George, 1979; Hopper and Hall, 1975; Ivy et al., 1985; Ivy et al., 1986; Klar et al., 1979; Rine et al., 1979; Rine and Herskowitz, 1987). The molecular mechanism by which the *SIR* genes act to repress transcription is unclear; none of the *SIR* proteins have been demonstrated to bind silencer sequence DNA (Buchman et al., 1988; Shore et al., 1987).

35

A null allele of either *NAT1* (N-terminal AcetylTransferase) or *ARD1* (Arrest Defective) causes

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several phenotypes, one of which is derepression of the
silent mating type locus *HML* (Mullen et al., 1989;
Whiteway et al., 1987). *NAT1* and *ARD1* appear to encode
an N-terminal acetyltransferase, however it is not known
5 whether the acetyltransferase activity acts directly in
silencing at *HML*.

S. cerevisiae harbors two copies of genes encoding
histone H4 (*HHF1* and *HHF2*), either of which alone is
10 sufficient for viability (Kim et al., 1988). In strains
with deletions of *HHF1* (*hhf1::HIS3*), single point
mutations in any of four consecutive amino acids
(residues 16-19) near the N-terminus of histone H4 (*HHF2*)
relieve transcriptional silencing at *HML*, with no other
15 apparent phenotypic consequence (Johnson et al., 1990;
Megee et al., 1990; Park and Szostak, 1990). These
results directly implicate chromatin in *HM* silencing.
Further evidence for the involvement of chromatin in
silencing is suggested by the inaccessibility of *HML* and
20 *HMR* to the HO endonuclease *in vivo* (Strathern et al.,
1982; Kostriken et al., 1983). Additionally, *in vitro*
nuclease sensitivity analysis of *HML* and *HMR* suggests
that the *HM* loci exist in a distinct chromatin structure
that is refractory to transcription in a *SIR* dependent
25 manner (Nasmyth, 1982).

The characteristics of position effect and *RAP1*
binding sites shared by telomeres and the *HM* loci
prompted the inventors to test whether the *SIR*, *HHF2*,
30 *NAT1*, and *ARD1* genes play a role in transcriptional
repression at yeast telomeres. The results of this
Example show that in addition to their roles in silencing
at the *HM* loci, the *SIR2*, *SIR3*, *SIR4*, *NAT1*, *ARD1*, and
HHF2 genes are required for the telomeric position effect
35 in *S. cerevisiae*.

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Mutations in any of these genes relieves transcriptional repression of either *URA3* or *ADE2* at two different telomeres. In contrast, mutations in *SIR1* did not alter repression at telomeres. These results suggest
5 that telomeres in *S. cerevisiae* exist in a heterochromatin-like structure; a structure composed of proteins which also function at similar chromosomal domains such as the *HM* loci. Based on the differences in silencing between telomeres, *HML*, and *HMR*, the inventors
10 suggest a hierarchy of chromosomal silencing exists within the yeast genome.

A. MATERIALS AND METHODS

15 1. Plasmid Constructions

Plasmid pADE2 contains the *ADE2* gene on a 3.6 kbp chromosomal *Bam*HI fragment from plasmid pL909 (obtained from R. Keil). Plasmid pΔADE2 was constructed by
20 replacing the internal 2.2 kbp *Hind*III fragment (contains all but the six C-terminal residues of the *ADE2* open reading frame; (Stotz and Linder, 1990) of plasmid pADE2 with the 3.8 kbp *Bam*HI-*Bgl*II fragment of pNKY51 which contains two direct repeats of the *Salmonella hisG* gene
25 flanking *URA3* (Alani et al., 1987). The *Hind*III and *Bam*HI ends, and the *Hind*III and *Bgl*II ends were blunt-ended with T4 DNA polymerase and ligated together, resulting in the destruction of these particular restriction sites. Thus, pΔADE2 contains a 5.2 kbp *Bam*HI
30 fragment with about 700 bp of homology to sequences upstream and downstream of the *ADE2* gene flanking the 3.8 kbp *Bam*HI-*Bgl*II (*hisG-URA3-hisG*) fragment from pNKY51.

A 2.4 kbp *Hind*III fragment from plasmid pJR104
35 (obtained from J. Rine) which contains the 5' end of the *SIR3* gene was inserted into pVZ1 to yield plasmid pH3SIR3. Plasmid pH3SIR3 was digested with *Bgl*II to

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excise a 600 bp fragment in the *SIR3* coding sequence, which was replaced with a 1.8 kbp *Bam*H1 fragment containing the *HIS3* gene. The resulting plasmid was p Δ SIR3::*HIS3*.

5

2. Yeast Strains and Methods

Media used for the growth of *S. cerevisiae* were described previously (Gottschling et al., 1990; Example 10 I). *S. cerevisiae* were transformed by the lithium acetate procedure (Ito et al., 1983) or by electroporation in the presence of sorbitol (Becker and Guarente, 1991).

15 The *URA3* gene was placed adjacent to the telomere sequence (TG₁₋₃)_n on the left end of chromosome VII (UCC1-UCC5, UCC16, UCC18, UCC25, UCC128, UCC2031-UCC2036), or the right end of chromosome V (UCC31-UCC35); no telomere associated sequences (i.e.: X and Y' elements (Chan and 20 Tye, 1983a; Chan and Tye, 1983b)) were present. Alternatively, the *ura3-52* or *ura3-1* allele (at the normal *URA3* locus on chromosome V in the parent strains) was converted to *URA3*⁺ (UCC6-UCC10, and UCC129), or *URA3* was inserted into the *ADH4* locus about 20 kbp from the 25 telomere on VII-L (UCC11-UCC15).

Strains UCC5, UCC6, UCC12, and UCC35 were derived from DBY703; UCC1, UCC7, UCC11, and UCC31 were derived from JRY1705; UCC2, UCC8, UCC13, and UCC32 were derived 30 from JRY1706; UCC3, UCC9, UCC14, and UCC33 were derived from JRY1264; UCC4, UCC10, UCC15, and UCC34 were derived from JRY1263. Strain UCC18 was derived from W303-1a; UCC16 was derived from AMR1; UCC25 was derived from JRM5. UCC128 and UCC129 were derived from YDS73; strain UCC2031 35 was derived from LJY153, UCC2032 from LJY405I, UCC2033 from LJY412I, UCC2034 from LJY421I, UCC2035 from LJY305TR1, UCC2036 from LJY305T. Plasmids and methods

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for these constructions are described in Example I and Gottschling et al. (1990).

Strains UCC46 (*SIR*⁺), UCC47 (*sir1*), and UCC48
5 (*sir4*), which were derived from strains DBY703, JRY1705,
and JRY 1263, respectively, harbor an *ade2Δ*. The *ade2Δ*
was made by transformation of strains DBY703, JRY1705,
and JRY1263 with plasmid pΔADE2 digested with *Bam*HI,
followed by selection for URA⁺ transformants. In these
10 transformants the ADE2 open reading frame has been
replaced (all but the six C-terminal residues were
deleted) with a DNA fragment containing two direct
repeats of the *Salmonella hisG* gene flanking URA3. Loss
of URA3 by recombination between the two *hisG* repeats
15 within the *ade2* locus was screened for by 5-FOAR (Alani
et al., 1987).

Strains UCC84, UCC86, and UCC88, derived from UCC46,
UCC47, and UCC48, respectively, and strains UCC97, UCC98
20 and UCC99, derived by transformation of strains W303-1a,
AMR1, and JRM5, respectively, have a functional ADE2 gene
located adjacent to the chromosome VII-L telomere (ADE2-
TEL) (Example I); no telomere associated sequences (i.e.:
X and Y' elements (Chan and Tye, 1983a; Chan and Tye,
25 1983b)) were present. Strains UCC2037-UCC2042, derived
from strains LJY153, LJY405I, LJY412I, LJY421I, LJY305T,
and LJY305TR1, respectively, were constructed in the same
manner to place ADE2 adjacent to telomere VII-L.

30 Strain UCC121 was derived from W303-1a by
transformation with a 3.6 kbp *Bam*HI ADE2⁺ fragment and
selection for ADE⁺ transformants. Strain UCC120 was
constructed by introduction of plasmid pJR531 (Kimmerly
and Rine, 1987) which had been digested with *Sph*I and
35 *Eco*RV into UCC97, and selection for HIS⁺ transformants.
Strain UCC131 was constructed by introduction of

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pASIR3::HIS3 which had been digested with *EcoRI* into UCC84, and selection for HIS⁺ transformants.

Strains UCC122-UCC125, UCC138, and UCC139 were constructed by transformation of strains UCC16, UCC18, UCC19, UCC21, UCC128, and UCC129, respectively, with plasmid pKL1. Plasmid pKL1 contains the *SIR1* gene on a 2 μ -based vector which contains *TRP1* for selection (Stone et al., 1991).

The expected structures of the various chromosomal constructs were confirmed by gel electrophoresis followed by DNA blot hybridization analyses. The *sir*⁻ phenotypes of strains UCC130 and UCC131 were confirmed by their inability to mate (Sprague, 1991).

3. Quantification of 5-FOA Resistance

Cells from isolated colonies grown on rich medium for 2-3 days at 30° were inoculated into liquid medium containing (100mg/L) uracil. When these cultures reached mid-log phase, serial dilutions were plated onto synthetic complete medium or medium containing 5-FOA (Example 1; Gottschling et al., 1990). 5-FOA resistance was determined as the average ratio of colonies formed on 5-FOA medium to colonies formed on complete medium, from a minimum of three independent trials, using different colony isolates for each trial. The number of colonies on a plate was determined after 3-4 days of growth at 30°C. Alternatively, colonies of strains grown on rich medium two to three days were suspended in H₂O, and ten-fold serial dilutions were plated as described above. For some strains, selection for TRP⁺ was required to maintain episomal plasmids; these strains were grown on synthetic medium lacking tryptophan three to four days and colonies were suspended in H₂O, serially diluted, and

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plated as above on synthetic medium lacking tryptophan or on 5-FOA medium lacking tryptophan.

4. Analyses of Nucleic Acids from *S. cerevisiae*

5

Preparation and analyses of nucleic acids were as in Example I, except that some DNA blot hybridization analyses were carried out using the Genius system from Boehringer Mannheim following the manufacturer's procedures.

10

B. RESULTS

1. *SIR2*, *SIR3*, and *SIR4* Maintain Transcriptional Repression at Telomeres

15

An isogenic set of *sir⁻* strains with the *URA3* gene located at one of four different chromosomal sites was constructed: adjacent to telomere VII-L or V-R, at its normal chromosomal location, or at a second non-telomeric site (*ADH4*, ~20 kbp from telomere VII-L). *URA3* expression was measured by two criteria: resistance to 5-fluoroorotic acid (5-FOA^R), and *URA3* mRNA levels as determined by RNA blot hybridization analysis. 5-FOA is converted into a toxic metabolite by the *URA3* gene product, such that cells expressing normal levels of the *URA3* gene product are killed on media containing 5-FOA, whereas *ura3⁻* cells are resistant to 5-FOA (5-FOA^R) (Boeke et al., 1987). Cells with *URA3* near a telomere form colonies on 5-FOA medium, yet cells within these 5-FOA^R colonies can grow in the absence of uracil, indicating that genetically identical cells can switch from a clonally inherited repressed state to a transcriptionally active state (Gottschling et al., 1990).

35

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Consistent with these earlier results, when the *URA3* gene was located adjacent to either the VII-L or V-R telomere in a *SIR*⁺ strain, a significant fraction of cells were resistant to 5-FOA (0.62 for UCC5, 0.15 for UCC35), and cells from 5-FOA^R colonies retained the ability to form colonies on medium lacking uracil. Similar results were obtained with the *sir1* strain, indicating that expression of the telomeric *URA3* gene is repressed in a subset of cells in these strains, and that the *SIR1* gene product is not required for repression.

In contrast, a telomeric *URA3* gene was not repressed in cells that were *sir2*, *sir3*, or *sir4*. The frequency of 5-FOA^R colonies arising from these strains ($\sim 10^{-7}$) was equivalent to that seen for all strains with *URA3* at its normal chromosomal locus or at the *ADH4* locus. Mutations in the *SIR* genes had no effect on the 5-FOA resistance of cells having *URA3* at either of these non-telomeric loci.

RNA blot hybridization analysis shows that sensitivity to 5-FOA as a result of the *sir*⁻ mutations was a reflection of mRNA levels from the telomeric *URA3* gene. No *URA3* mRNA was detectable in *SIR*⁺ or *sir1* strains which had *URA3* at the telomere and were grown under non-selective conditions ("uracil +"), even when the autoradiograph was greatly overexposed. *URA3* mRNA was only detectable in the *SIR*⁺ or *sir1* strains when they were grown to select for telomeric *URA3* expression ("uracil -"), though this level was significantly lower than when *URA3* was at its normal chromosomal locus.

In sharp contrast, the telomeric *URA3* gene produced high levels of mRNA in *sir2*, *sir3*, and *sir4* strains. These levels were comparable to those from *URA3* at its normal chromosomal locus. The *sir*⁻ mutations had no effect on *URA3* expression at its normal chromosomal locus or when inserted within the *ADH4* locus. These data

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indicate that the telomeric position effect on *URA3* expression mediated by *SIR2*, *SIR3*, and *SIR4* is at the level of transcription.

5 To demonstrate that the *SIR* requirement for the telomeric position effect was not gene specific, *sir⁻* strains were constructed with the *ADE2* gene located at the VII-L telomere, or at its normal locus. The *ADE2* gene provides a visual color assay for its expression;
10 *ADE2⁺* strains form white colonies, while *ade2⁻* strains form red colonies (Roman, 1956). Example I shows that a *SIR⁺* strain containing a single copy of *ADE2* at a telomeric locus exhibited phenotypic variegation of *ADE2*, manifested as red-and-white sectorized colonies. Here it
15 was found that strains with the telomeric *ADE2* that were *SIR⁺* or *sir1* formed red and white variegated colonies, indicating that *ADE2* was repressed in a subset of the cells within these colonies. The *sir2*, *sir3*, and *sir4* strains formed entirely white colonies, demonstrating
20 that the telomeric *ADE2* gene was not repressed (for *sir2* and *sir3*). These results confirm that the *SIR2*, *SIR3*, and *SIR4* genes are required for maintaining transcriptional repression at telomeres, in addition to silencing the *HM* loci (Rine and Herskowitz, 1987).
25

2. Single Point Mutations in Histone H4 Relieve Transcriptional Repression at Telomeres

Single point mutations in any of four consecutive
30 amino acids (residues 16-19) near the N-terminus of histone H4 (*HHF2*) relieve transcriptional silencing at *HML* (Johnson et al., 1990; Megee et al., 1990; Park and Szostak, 1990). *URA3* or *ADE2* was placed at the VII-L telomere in isogenic strains that carried a single copy
35 of either the wild-type histone H4 (*HHF2*), or a mutated copy of *HHF2*. Three such point substitution mutations, all of which derepress *HML*, were tested: a change of lys-

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16 to either gly-16 or gln-16, and a change of arg-17 to gly-17.

Each strain that contained one point mutation in histone H4 exhibited derepression of telomeric *URA3* transcription as shown by their inviability on 5-FOA. When *ADE2* was near the telomere in strains with these same histone H4 mutations, colonies were completely white, once again indicating derepression of the telomeric gene. Thus single point mutations at residues 16 or 17 in histone H4 which replace the wild-type basic amino acid with an uncharged residue, result in relief of the telomeric position effect.

There is genetic evidence that *SIR3* interacts with histone H4 to silence genes at *HML* (Johnson et al., 1990). Alleles of *sir3* (e.g. *sir3R1*) have been identified that can partially suppress the *HML* silencing defect caused by certain point mutations in histone H4 (e.g.: lys-16 to gly-16). *URA3* was introduced at the VII-L telomere in an isogenic pair of strains which were either *HHF2-gly16, SIR3⁺* (UCC2036) or *HHF2-gly16, sir3R1* (UCC2035). No suppression by *sir3R1* was observed at the telomere as judged by complete sensitivity to 5-FOA. Equivalent strains with *ADE2* at the telomere produced no red sectored colonies, supporting the conclusion that the *sir3R1* allele could not restore repression at the telomere in an *HHF2-gly16* strain.

3. *NAT1* and *ARD1* are Required for the Telomeric Position Effect

A null mutation of either *NAT1* or *ARD1* causes derepression of the silent mating-type locus *HML* (Mullen et al., 1989; Whiteway et al., 1987). *URA3* or *ADE2* was introduced at the VII-L telomere into each member of a set of isogenic strains that was either *nat1*, *ard1*, or

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wild-type for both genes. The sensitivity to 5-FOA of *nat1* and *ard1* strains was equivalent to that observed for *sir2*, *sir3*, and *sir4* and the point mutants in histone H4. Thus no position effect was observed for a telomeric *URA3* gene in *nat1* or *ard1* cells. Likewise, the telomeric *ADE2* gene was not repressed in the *nat1* and *ard1* strains as these strains formed entirely white colonies.

4. Overexpression of *SIR1* does not restore position effect at telomeres

Overexpression of *SIR1* partially suppresses the mating defects of *MATa* strains containing *nat1* or *ard1* mutations, or certain *sir3* or *HHF2* alleles by re-establishing silencing at *HML α* (Stone et al., 1991). The inventors tested whether *SIR1* overexpression could restore silencing of a telomere-linked gene in a *nat1* or *sir3::LEU2* strain. Plasmid pKL1 (Stone et al., 1991) which contains *SIR1* on a 2 μ -based vector was transformed into strains which were *nat1*, *sir3*, or wild-type and have *URA3* located at telomere VII-L or at the normal *URA3* locus. As expected, a significant fraction of cells of strain UCC123 (wild-type, *URA3*-TEL / pKL1) were resistant to 5-FOA. However, the *nat1* and *sir3* strains which have *URA3* at telomere VII-L and harbor pKL1 continue to be sensitive to 5-FOA, as are the strains with *URA3* at its normal chromosomal locus. Thus the overexpression of *SIR1* does not restore silencing at telomeric loci in *nat1* or *sir3* strains. These results are consistent with the results presented above, indicating that *SIR1* plays no role in transcriptional silencing at telomeres.

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C. DISCUSSION

1. Similarities and Differences in Position
Effects at Telomeres and the *HM* loci

5 This example shows that the *SIR2*, *SIR3*, *SIR4*, *HHF2*,
NAT1, and *ARD1* genes are required for the position effect
at telomeres in *S. cerevisiae*. Consequently, it implies
that these gene products constitute a general mechanism
10 for silencing chromosomal domains in *S. cerevisiae*. In
view of the results presented here, it is interesting to
note that both *HML* and *HMR* are located quite close to the
termini of chromosome III, ~12 kbp (Button and Astell,
1986) and ~25 kbp (Yoshikawa and Isono, 1990),
15 respectively. When *HML* is present on a circular plasmid
or a ring chromosome III derivative, deletion of *HMLE* or
HMLI results in derepression of *HML* (Feldman et al.,
1984; Strathern et al., 1979). However, these mutated
HML loci are fully silenced when present at the normal
20 telomeric *HML* locus (Mahoney and Broach, 1989) suggesting
the proximity of *HML* to the telomere may facilitate full
repression of this locus.

There was no detectable change in the
25 telomere-specific position effect in *sir1* strains or in
strains with *SIR1* on a high copy plasmid. Since both of
these genotypes have an effect on *HML* and *HMR*, the
inventors conclude that *SIR1* function is specific to
silencing of the *HM* loci. Single-cell analysis of *sir1*
30 strains indicates that a mixed population of cells exists
with ~20% of cells being transcriptionally silent at *HML*
and the remainder being transcriptionally active at *HML*;
the transcriptional state is clonally inherited, though
cells switch between transcriptionally active and
35 repressed states at a low frequency (Pillus and Rine,
1989).

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The inventors have found that epigenetic switching between transcriptional states occurs at telomeres in *SIR⁺* (and *sir1*) strains, analogous to that observed at *HML* in *sir1* mutants (Example I; Pillus and Rine, 1989).

5 The inventors therefore propose that *SIR1* provides complete silencing at *HML* and *HMR* by preventing switching from the silent to the active transcriptional state. The *HM* loci is thus proposed to contain elements through which *SIR1* acts, which are absent from chromosomal
10 termini (e.g.: the A and B elements (Brand et al., 1987)). In support of this, a recent study has identified deletions at *HMLE* which result in epigenetic switching of transcriptional states at *HML* (Mahoney et al., 1991).

15

A number of differences have been observed between silencing at telomeres, *HML*, and *HMR*, which may yield insights into the functional organization of the silent loci. As indicated above, the epigenetic switching of
20 *HML* expression in *sir1* strains is very similar to the expression of a telomeric gene in a *SIR⁺* (or *sir1*) strain, indicating that elements through which *SIR1* can act to fully silence *HML* are present at *HML* (and probably *HMR*) but not at telomeres. Also, while a *sir1* mutation
25 has only a slight effect at either *HM* locus, and a mutation in *nat1* alone derepresses *HML* but not *HMR* (Mullen et al., 1989), the *sir1*, *nat1* double mutant is completely derepressed at *HMR*, suggesting that additional mechanisms of silencing exist at *HMR* compared to *HML* (or
30 telomeres) (Stone et al., 1991). Deletion of *NAT1* or *ARD1* results in significant derepression of *HML* but not *HMR* (Whiteway et al., 1987); however, deletion of the *RAP1* binding site at *HMRE* results in derepression of *HMR* in *nat1* or *ard1* strains (Stone et al., 1991), again
35 indicating that redundant silencing mechanisms exist at *HMR* compared to *HML* and telomeres.

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Lastly, *sir3R1* partially restores *HML* silencing in a *HHF2-gly16* strain (mating efficiency is restored from $\sim 10^{-5}$ to $\sim 10^{-1}$; (Johnson et al., 1990)), but does not restore telomeric silencing. This may be explained if suppression of *HHF2-gly16* by *sir3R1* is facilitated by the presence of a redundant silencing mechanism(s), such as that mediated by *SIR1*. Thus the inventors suggest that telomeres exhibit a basal level of transcriptional repression, and that silencing at *HML* and *HMR* is based on the same mechanism(s), but is strengthened and regulated by the presence of additional silencer elements.

2. How does the telomeric position effect occur?

Little is known about the specific mechanism by which the *SIR*, *HHF2*, *NAT1*, and *ARD1* gene products act in transcriptional silencing, however the available evidence suggests that they modify chromatin structure (Nasmyth, 1982). Single point mutations in histone H4 completely relieve the telomeric position effect and thus provide the best evidence that chromatin structure is intimately involved in telomeric silencing. Mutations in any of four contiguous amino acids (residues 16-19) in the N-terminus of histone H4 result in derepression at *HML* (Johnson et al., 1990; Megee et al., 1990; Park and Szostak, 1990); these four positively charged amino acids are conserved throughout eukaryotes, and are sites of post-translational modifications (van Holde, 1989). Significantly, correlative studies note that the modifications (e.g. acetylation and phosphorylation) on histone H4 are associated with the transcriptional status of the chromatin (van Holde, 1989).

In yeast, suppressors of the histone H4 point mutations, which restore silencing, map as compensatory changes in the *SIR3* gene, thus providing evidence that *SIR3* interacts with chromatin (Johnson et al., 1990). In

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addition, *SIR2* has been shown to suppress intrachromosomal recombination between rDNA repeats, supporting the idea that *SIR2* may play a general role in chromatin organization (Gottlieb and Esposito, 1989).

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NAT1 and *ARD1* apparently encode two subunits of a yeast N-terminal acetyltransferase which acetylates histone H2B along with at least twenty other proteins (Mullen et al., 1989) which may play a direct role in silencing by acetylation of H2B.

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It has been reported that *SIR4* shares sequence similarity with the coiled-coil domains of human nuclear lamins A and C (Diffley and Stillman, 1989). These domains facilitate polymerization of lamins into the lamina, which lines the nuclear envelope. Taking into account the cytological observations in interphase nuclei which indicate telomeres are located at the nuclear periphery it is plausible that the putative polymerization domain of *SIR4* is associated with the nuclear lamina and might therefore mediate binding of telomeres to the nuclear envelope. Since the *SIR4* gene product is believed not to bind DNA directly (Buchman et al., 1988; Shore et al., 1987), an interaction between *SIR4* and a telomere binding protein (e.g. RAP1) may enable an association between telomeres and the nuclear envelope. It is noteworthy that purified mammalian nuclear lamins A and C bind *in vitro* to synthetic oligonucleotides containing mammalian telomere repeat sequences (Shoeman and Traub, 1990). Thus attachment of telomeres, as well as other chromosomal loci or regions, to the nuclear envelope may be a component of nuclear organization, and might therefore affect local gene expression (Alberts et al., 1989; Blobel, 1985).

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The position effect at *S. cerevisiae* telomeres may reflect a general feature of eukaryotic telomeres. In

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Drosophila, stable transposition of the *white* gene to a position near a telomere results in a mottled eye color phenotype (Levis et al., 1985), which is consistent with transcriptional repression of *white* in some cells.

5 Cytological studies in a number of organisms indicate that telomeres are organized into heterochromatin (Lima-de-Faria, 1983; Traverse and Pardue, 1989). While heterochromatin is defined cytologically as a region of the chromosome which remains condensed in interphase, it
10 also displays two distinctive traits: late DNA replication, and the ability to repress transcription of euchromatic genes placed nearby (Eissenberg, 1989; Henikoff, 1990; Spofford, 1976; Spradling and Karpén, 1990). *S. cerevisiae* telomeres possess both of these
15 hallmarks of heterochromatin (Example I; McCarroll and Fangman, 1988). The *SIR2*, *SIR3*, *SIR4*, *HHF2*, *NAT1*, and *ARD1* products may be intimately involved with the organization of regions of yeast chromosomes into heterochromatin or heterochromatin-like structures.
20 Because telomeres and histones are highly conserved structurally and functionally among eukaryotes, it seems quite likely that the mechanism of transcriptional repression functioning in *S. cerevisiae* is also utilized in multi-cellular eukaryotes.

25

EXAMPLE III

Silent Domains are Assembled Continuously from the
Telomere and are Defined by Promoter Distance and
Strength and *SIR3* Dosage

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The eukaryotic genome is organized into regions distinct in their structure and function. Heterochromatin, which defines one such structural region, is condensed throughout the cell cycle, while its
35 counterpart, euchromatin, is more diffuse in appearance during interphase (Heitz, 1928, as cited in Brown, 1966). Chromosomal regions also differ functionally since the

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expression of a eukaryotic gene can be profoundly affected by its chromosomal position. This phenomenon, chromosomal position effect, is observed in many eukaryotes (Lima-de-Faria, 1983) and has been extensively
5 studied in *Drosophila melanogaster* (Lewis, 1950; Baker, 1968; Spofford, 1976). When genetic rearrangements place euchromatic segments of the genome into or near heterochromatin, the expression of a translocated
euchromatic gene is altered in a population of cells:
10 some cells express the gene, while others do not. Thus a mosaic or variegated phenotypic pattern is produced.

Chromosomal position effects phenomena can spread over great distances in the genome; e.g., in *Drosophila*,
15 genes located as far away as 80 chromosome polytene bands (~2000 kbp) are still subject to position-effect variegation (PEV) (Demerec, 1940). This spreading effect is thought to reflect the dynamic nature of assembly of heterochromatin over a locus (Zuckerkindl, 1974;
20 Spofford, 1976). When heterochromatin assembles far enough to include a locus, the gene within it is inactivated.

In *Saccharomyces cerevisiae*, chromosomal domains
25 have been identified that exert position effect: the cryptic mating-type loci, *HML* and *HMR*, and telomeres (Laurenson and Rine, 1992; Sandell and Zakian, 1992). Genes located near or within these domains may be transcriptionally silenced and exhibit phenotypic
30 variegation (Klar et al., 1981; Nasmyth, et al. 1981; Schnell and Rine, 1986; Mahoney and Broach, 1989; Example I). At least six modifiers of position effect are shared between the *HM* loci and telomeres. A mutation in *SIR2*,
SIR3, *SIR4*, *NAT1*, *ARD1*, or *HHF2* (which encodes histone
35 H4) reduces or abolishes silencing at telomeres, *HML*, and *HMR* (Hopper and Hall, 1975; Haber and George, 1979; Klar et al., 1979; Klar et al., 1981; Ivy et al., 1986; Rine

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and Herskowitz, 1987; Whiteway et al., 1987; Kayne et al., 1988; Mullen et al., 1989; Megee et al., 1990; Park and Szostak, 1990; Example II; Aparicio et al., 1991).

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The involvement of histone H4, and the observation that the *HM* loci and telomeres are refractory to DNA modifications *in vivo* in a *SIR*-dependent manner, point to chromatin structure as being involved in silencing the *HM* loci and telomeres. Specifically, this chromatin structure is thought to hinder access of transcription factors to these loci (Nasmyth, 1982; Kostriken et al., 1983; Klar et al., 1984; Gottschling, 1992; Singh and Klar, 1992).

15

Spreading of position effect also occurs in yeast (Abraham et al., 1984; Feldman, et al. 1984). Genes located up to ~4.9 kbp from a telomere still are subject to position effect, whereas no silencing is detected at loci ~20 kbp from the chromosome end (Gottschling et al., 1990). Additionally, insertion of a 30 kbp Ty-array between the E and I sites (*cis*-elements required for silencing) at *HMLa* relieves silencing at this locus. However silencing is re-established when this array is reduced to a single 7 kbp Ty (Mastrangelo et al., 1992). Thus there is a limit to the size of silenced domains at both *HM* loci and telomeres.

25

Telomeric silencing in yeast provides an excellent opportunity to study the spread of position effect in a eukaryote, particularly because the initiation site of position effect is known to be the end of the chromosome (Example I). In this Example, a quantitative method to examine telomeric position effect was used to identify parameters that modulate spreading. The results provide a molecular and mechanistic insight into the propagation

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of silencing in yeast, as well as the functional organization of silent chromosomal domains.

A. METHODS

5

1. Construction of Plasmids

The set of plasmids used to insert the *URA3* gene at various positions along V-R was constructed as follows, starting with plasmid pB610H (obtained from C. Newlon). Plasmid pHSS6TG carries a telomeric repeat sequence (derived from pYTCA-2; Example I) inserted between the *EcoRI* and *BamHI* restriction sites of plasmid pHSS6 (Seifert et al., 1986). Orientation of the telomeric sequence is such that digestion of pHSS6TG with *EcoRI* will yield an end that is a substrate for telomere formation in yeast. A 7.3 kbp *BamHI* fragment from plasmid pB610H was ligated into the *BamHI* site of pHSS6TG. Next, a 7.4 kbp *NotI* fragment of this new plasmid, carrying unique V-R sequences adjacent to a telomeric (TG₁₋₃)_n repeat, was cloned into the *NotI* site of pVZ1 (Henikoff and Eghtedarzadeh, 1987), generating pSC1. Plasmids pVURAH2(+) and pVRURAH2(-) were constructed by inserting a 1.2 kbp *HindIII* fragment containing *URA3* into the "H₂" site of pSC1 partially digested with *HindIII*. *URA3* transcriptional orientation is denoted (+) when transcription is toward the telomere and (-) when toward the centromere. *URA3* was cloned in a similar way into the "H₃" and "H₄" *HindIII* restriction sites, generating plasmids pVURAH3(+), pVURAH3(-), pVURAH4(+) and pVURAH4(-), respectively.

The *HIS3* gene was isolated from plasmid pHIS3 (Struhl, 1985; Example I) by amplification using the polymerase chain reaction (Innis et al., 1990), using the following primers : 5' oligo
5' CCGGATCCTGCCTCGGTAATGATTTTCATTTTTT 3' (SEQ ID NO:13);

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3' oligo 5' CCGGATCCTCTCGAGTTCAAGAGAAAAAAAAGAAA 3' (SEQ ID NO:14). Restriction sites for *Bam*HI, which were placed at the ends of the oligonucleotides for convenient cloning, are underlined. Hence, the inventors refer to this DNA segment as "*HIS3 Bam*HI fragment".

Plasmids used to test for discontinuity of silenced chromosomal domains along V-R were created as follows: pH1.5*HIS3*(+) and pH1.5*HIS3*(-) were constructed in two steps. First, a 1.5 kbp *Hind*III fragment of V-R chromosomal DNA was inserted into the *Hind*III site of pHSS6 to generate plasmid pHSS6(1.5). pHSS6(1.5) was then digested with *Kpn*I, blunt-ended, and ligated with the *HIS3 Bam*HI fragment which had its ends filled-in. A two-step process was also required to construct plasmids pVRUH2(-)HR1(+) and pVRUH2(-)HR1(-). Plasmid pVRUH2(-) was cut with *Xho*I and *Sal*I, and recircularized by ligation; a blunt-ended *HIS3 Bam*HI fragment was ligated into this plasmid which had been partially digested with *Eco*RI and blunted with T4 DNA polymerase. Plasmids pVRUH2(+)HR1(+) and pVRUH2(+)HR1(-) were constructed following the same procedure. Plasmids pYAHIS4-2(-) were made by cloning the *HIS3 Bam*HI fragment into the *Bam*HI site of pYA4-2 (Walton et al., 1986).

25

Plasmid pDPPR1-*HIS3* was constructed by replacing a 0.7 kbp *Bgl*II fragment containing the promoter region of *PPR1* (Kammerer et al., 1984), in plasmid pUC8-*PPR1* (obtained from R. Losson), with a 1.85 kbp *Bam*HI fragment from plasmid pHIS3. In plasmid pDPPR1::LYS2 the same *Bgl*II fragment was replaced by a blunt-ended 4.8 kbp *Hind*III-*Xba*I fragment containing *LYS2*, isolated from pDP6 (Fleig et al., 1986).

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Plasmid pVZ1DGCN4::TRP1 carries a deletion in the translation initiation region of *GCN4*. Plasmid pB238 (a derivative of plasmid p164 (Hinnebusch, 1985)) was

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digested with *Bam*HI and *Bgl*II, and a 0.8 kbp *Bam*HI fragment containing *TRP1* from YDpW (Berben et al., 1991) was ligated into it. A *Sal*I-*Eco*RI 3.2 kbp fragment of the resulting plasmid was then ligated into pVZ1 previously digested with *Eco*RI and *Sal*I, to create pVZ1DGCN4::*TRP1*.

The plasmid pVZJL38*TRP1*(+)*ADE2*(-) was used to insert *TRP1* and *ADE2* between *ADH4* and telomere VII-L. Plasmid pUC19-JL3 contains a 0.4 kbp *Eco*RI-*Hind*III fragment including the JL3 region from VII-L (Walton et al., 1986). This plasmid was digested with *Eco*RI, its ends were made blunt, and the linearized plasmid was treated with *Hind*III. The JL3 region was ligated into plasmid pVZ1 previously digested with *Hinc*II and *Hind*III. Plasmid pVZJL38 was constructed by digesting the resulting plasmid, pVZJL3, with *Sma*I and *Eco*RI; an ~0.8 kbp *Eco*RI-*Hind*III fragment from plasmid pUC19-JL8 (Walton et al., 1986), with only its *Hind*III end made blunt, was ligated into the plasmid. A 1.45 kbp *Eco*RI fragment from plasmid YRp7 containing the *TRP1* gene (Struhl et al., 1979), was then inserted into this new plasmid, pVZJL38. The resulting plasmid, pVZJL38*TRP1*(+), was digested with *Bgl*II and a 3.6 kbp *Bam*HI fragment containing *ADE2* was inserted (Gottschling et al., 1990). Plasmid pVZJL38*TRP1*(+)*ADE2*(-) has *ADE2* inserted in the opposite transcriptional orientation as *TRP1*.

YE*pSIR3* (pKAN63) carries a ~7 kbp *Bam*HI genomic insert containing *SIR3* and flanking chromosomal sequences (Ivy et al., 1986), cloned into YE*p13* (Broach et al., 1979). CEN-*SIR3* (pHR62-16) contains a 3.7 kbp *Hpa*I fragment of plasmid pKAN63, encompassing *SIR3* and its putative transcriptional regulatory elements (Shore et al., 1984), inserted into the *Sma*I restriction site of plasmid pRS314 (Sikorski and Hieter, 1989). Plasmid-23 (2*m-SIR3*) carries the same *SIR3* fragment cloned into

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pHR59-33 (2m), a derivative of pRS424 (Christianson et al., 1992) in which the *Cla*I site was deleted.

Plasmid pHR49-1 was constructed by inserting a 1.2 kbp *Bam*HI fragment containing *HIS3* from YDpH (Berben et al., 1991) into the *Bgl*II site of pRS316-SIR1 (obtained from Lorraine Pillus), which contains *SIR1* and flanking genomic sequences. All other plasmids used for strain construction have been described previously (Ivy et al., 1986; Kimmerly and Rine, 1987; Examples I and II).

DNA manipulations were performed as previously reported (Sambrook et al., 1989; Example I). *E. coli* strains MC1066 (*r⁻ m⁻ trpC9830 leuB600 pyrF::Tn5 lacDX74 strA galU galK*) (Casadaban et al., 1983), JF1754 (*r⁻m⁻ leuB metB hisB*) (Himmelfarb et al., 1987) and TG1 (*supE hsdD5 thiD(lac-proAB) F'[traD36 proAB⁺ lacI^q lacZDM15]*) (Sambrook et al., 1989) were used as plasmid hosts. Media for bacterial strains were prepared as described (Sambrook et al., 1989). Complementation of bacterial mutations by homologous yeast genes was used when applicable.

2. Yeast Strains and Methods

Media used for the growth of *S. cerevisiae* were described in Example I; all cultures were grown at 30°C. Yeast transformation was performed by electroporation in the presence of sorbitol (Becker and Guarente, 1991) or the lithium acetate procedure (Schiestl and Gietz, 1989). 5-FOA resistance (5-FOA^R) was determined as described in Example II. Yeast strains manipulations were carried out as described (Rose et al., 1990).

Strains UCC500-505 were constructed by transformation of YPH250 (Sikorski and Hieter, 1989) with

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*Bam*HI-digested plasmids pVURAH2(+), pVURAH2(-), pVURAH3(+), pVURAH3(-), pVURAH4(+), and pVURAH4(-), respectively. Strains UCC506-511 were constructed by transformation of strain YPH250 with the same plasmids digested with *Not*I. In both cases, Ura⁺ colonies were selected. *ppr1*⁻ derivatives of these strains were constructed by transformation with *Eco*RI digested pDPPR1-HIS3, and selection for His⁺ transformants.

URA3 was inserted into the *ADH4* locus (about 20 kbp from telomere VII-L) of YPH250 to yield UCC1003, as described (Gottschling et al., 1990). UCC3248, UCC3249 and UCC3250 are derivatives of UCC1001 (Gottschling, 1992) that are *sir2::HIS3*, *sir3::HIS3* and *sir4::HIS3*, respectively, and were created by transformation as described (Kimmerly and Rine, 1987; Example II). A *sir1::HIS3* derivative of UCC1003 (UCC3243) was constructed by transforming UCC1003 with *Cla*I and *Sma*I digested pHR49-1.

Plasmid pH1.5HIS3(+) was digested with *Not*I and transformed into UCC506 and UCC507 to make UCC2515 and 2517, respectively. pH1.5HIS3(-) was transformed in the same way into UCC506 and UCC507, to generate UCC2516 and UCC2518, respectively. Strains UCC2524-2527 were derived from YPH250 after transformation with the various pVRUH2(+/-)HR1(+/-) constructions digested with *Sph*I and *Not*I. UCC1005 is derived from YPH250 (Sikorski and Hieter, 1989) by transformation with pVRURA3TEL, as described (Gottschling et al., 1990). UCC1005 was transformed with pYAHIS4-2(-) that had been digested with *Eco*RI and *Sal*I, yielding strain UCC2509. Strain UCC2528 carries a telomeric URA3 at the VII-L telomere; it was created by transformation of YPH500 (Sikorski and Hieter, 1989) with pVII-L URA3-TEL (Example I).

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The UCC2535 strain was created by transforming YPH250 with pVRUH2(-)HR1(+), selecting for His⁺ transformants, and then screening for Ura⁻ cells. URA3 was integrated at the ADH4 locus of UCC2535 by transformation with padh4::URA3, as described (Gottschling et al., 1990), generating strain UCC2585. UCC2536, a meiotic segregant of a cross between UCC2528 and UCC2535, carries HIS3 on V-R and URA3 on VII-L. ppr1⁻ gcn4⁻ derivatives of the strains UCC2515-2518, 2524-2527, 2509, 2536 and 2585 were constructed by transformation with EcoRI digested pDPPR1::LYS2, and selection for Lys⁺ colonies; next, the GCN4 locus was disrupted by transformation with pVZ1DGCN4::TRP1 digested with NotI and SalI, yielding UCC2580-2583, 2576-2579, and 2589-2591.

The gamma-deletion method (Sikorski and Hieter, 1989) was used to introduce TRP1 and ADE2 between the JL3 and JL8 regions on VII-L (Walton et al., 1986). Plasmid pVZJL38TRP1(+)ADE2(-) was digested with BamHI and transformed into UCC1003 to yield strain UCC1035. The expected structures of the various chromosomal constructs were confirmed by Southern analysis as described in Examples I and II. All other strains have been described in Example I.

B. RESULTS

1. Silencing of URA3 Decreases with Increased Distance From the Telomere

In Example I, the inventors detected telomeric position effect (TPE) in *S. cerevisiae* 4.9 kbp from the left end of a modified chromosome VII (VII-L) by measuring the level of transcriptional repression of a telomere-proximal URA3 when various yeast genes were inserted between URA3 and the telomere. However, the

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effect of each inserted sequence on *URA3* expression was not exclusively dependent on the size of the insert. To better characterize the spread of TPE in *S. cerevisiae*, the inventors examined the expression of *URA3* as a
5 function of its distance from a representative telomere, without introducing any new sequences between *URA3* and the end of the chromosome.

A set of isogenic strains was created with *URA3*
10 placed at various distances from the right end of chromosome V (V-R); the normal chromosomal copy of *URA3* is non-functional in each strain. At each site of insertion, *URA3* was positioned in either transcriptional orientation. This set of strains may be divided into two
15 groups: those that maintained the original ~6.7 kbp telomere-associated Y' element of V-R, and those in which the Y' and some adjacent sequences were replaced with a new terminus of (TG₁₋₃)_n. These Y' elements are middle-repetitive DNA sequences found proximal to some but not
20 all yeast telomeres; their function is unknown (Olson, 1991).

Transcriptional repression as a function of distance from the chromosome end was analyzed by determining the
25 level of *URA3* silencing in each strain. The level of silencing in a population of cells is quantified by determining the fraction of cells capable of forming colonies on 5-fluoroorotic acid (5-FOA) medium; 5-FOA is lethal to cells expressing the *URA3* gene product (Boeke
30 et al., 1987). In the inventors' analysis, the ability of a cell to give rise to a colony on 5-FOA (5-FOA^R) indicates that when it was plated onto the medium, the cell contained little or no *URA3* gene product. Thus when *URA3* is telomeric, telomere-mediated transcriptional
35 repression enables the cell to grow on 5-FOA (Gottschling et al., 1990).

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Quantification of TPE spreading showed that, when the fraction of 5-FOA^R cells is plotted versus the distance of the *URA3* promoter from the telomere, a continuous gradient in frequency of silencing is observed, with the highest frequency occurring at the most telomere-proximal position. Repression was no longer detected when the *URA3* promoter was located 3.5 kbp away from the telomere. The steady decrease in frequency of repression with respect to promoter distance from the telomere suggested that the position of the *URA3* promoter was the key element in determining repression; transcriptional orientation with respect to the telomere did not appear to be significant in regulating *URA3* expression. Finally, in strains with a Y' element between the *URA3* gene and the V-R telomere (UCC500-505), no repression was detected at the tested distances of 10 kbp to 16 kbp from the telomere.

2. Absence of a Transactivator Increases the Extent of TPE Spreading

If promoter distance from the telomere is a primary determinant for governing TPE spreading, then weakening the promoter might result in an increase in spreading. To test this, *ppr1*⁻ derivatives of the strains described above, with *URA3* at various distances from the telomere, were created. PPR1 is a transactivator protein that enhances expression of the *URA3* gene (Loison et al., 1980; Roy et al., 1990). Repression was more frequent at each location of *URA3*, and detectable over a greater distance from the telomere in *ppr1*⁻ than in *PPR1*⁺ strains. Thus the range over which TPE spreads seems to be inversely related to the promoter strength of the gene being assayed. Similarly, deleting *GCN4*, the *HIS3* transactivator (Hope and Struhl, 1985; Hinnebusch, 1988), reduced the ability of strains carrying a telomeric copy

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of *HIS3* to form colonies on medium lacking histidine, indicating that this effect is not specific to *URA3*.

In the *ppr1⁻* strains with the Y' element present at V-R, a small fraction of 5-FOA^R cells were reproducibly observed in the two strains in which the *URA3* promoter is about 11 and 12 kbp from the telomere. Southern analysis revealed no change in chromosome structure between *URA3* and the telomere in these strains. These results contrast with the data for strains lacking the Y' element on V-R (UCC518-523), in which no repression was detected beyond ~6 kbp from the V-R telomere. Thus it seems that 6.7 kbp of Y' sequence has a greater ability to sustain telomere-dependent silencing than the same length of unique V-R sequence.

3. Overexpression of *SIR3* Enhances TPE Spreading

The gene products of *SIR2*, *SIR3*, and *SIR4* are required for TPE, and it has been postulated that one or more of them is a structural component of silent yeast chromatin (Nasmyth, 1982; Ivy et al., 1986; Marshall et al., 1987; Rine and Herskowitz, 1987; Alberts and Sternglanz, 1990; Johnson et al., 1990; Example II; Stone et al., 1991). To examine whether the normal cellular level of *SIR2*, *SIR3*, or *SIR4* limits the range of silent telomeric domains, the inventors tested whether introduction of multiple copies of the *SIR2*, *SIR3*, or *SIR4* genes would increase the spread of TPE. Only raising *SIR3* copy number enhanced position-effect spreading on telomere-adjacent genes. No phenotype was observed in strains transformed with a multicopy plasmid carrying *SIR2*. Increasing *SIR4* dosage relieved silencing on telomeric genes; a similar effect has been previously observed at a weakened *HMR* (Sussel and Shore, 1991).

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The effect of *SIR3*-overexpression was quantified in the previously described sets of strains. Increased dosage of *SIR3* raised the frequency of *URA3* silencing in each strain. In *ppr1⁻* strains overexpressing *SIR3* on a high-copy plasmid (YE*pSIR3*), *URA3* was frequently silenced 5 16 kbp from the telomere (with a Y'), while in cells with vector alone (YE*p13*) no significant silencing was detectable beyond 4 kbp. Similar results were obtained in *PPR1⁺* strains transformed with YE*p13* or YE*pSIR3*, 10 although as expected from the data presented in the previous section, *URA3* transcription was somewhat less frequently repressed than in the *ppr1⁻* strains. Again, the presence of a Y' element appeared to facilitate TPE spreading over longer distances than unique chromosomal 15 sequences.

Extrapolation of the "YE*pSIR3* with Y'" curve suggested that TPE spreading should extend inward ~25 kbp from the end of chromosome V-R in the *SIR3*-overexpressing 20 strains. Consistent with this estimate, *URA3* was repressed at 22 kbp from the VII-L telomere when *SIR3* was overexpressed, but *URA3* expression was not affected at its normal locus, ~120 kbp from telomere V-L (Mortimer et al., 1992). No increase in telomeric silencing was 25 detected in strains transformed with plasmids carrying mutant alleles of *SIR3*, indicating that propagation of telomeric silencing is dependent on functional *SIR3*. These results are consistent with *SIR3* being a limiting component required to assemble repressive telomeric 30 chromatin.

If *SIR3* is indeed limiting, the spread of TPE should be very sensitive to *SIR3* gene dosage. This hypothesis was tested in *ppr1⁻* strains transformed with *SIR3* carried 35 either on a centromeric (CEN-*SIR3*) or a multicopy plasmid (2m-*SIR3*), or with the vectors alone. With a single-copy plasmid (CEN-*SIR3*), the spreading effect was indeed less

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enhanced than with a high-copy plasmid (2m-SIR3), but greater than with either vector alone. Hence, the results indicate that *SIR3* dosage limits the spread of yeast telomeric position-effect.

5

4. Increased *SIR3* Dosage Cannot Suppress the Requirements of *SIR2*, *SIR4*, *NAT1*, *ARD1*, and Histone H4 for TPE

10 In addition to *SIR3*, the gene products of *SIR2*, *SIR4*, *NAT1*, *ARD1* and *HHF2* (histone H4) are required for transcriptional silencing at telomeres (Example II). The inventors tested whether the increased dosage of *SIR3* could restore TPE in cells deficient for these other
15 proteins. Strains containing *URA3* adjacent to the VII-L telomere and defective in each of the aforementioned genes, were transformed with a high-copy *SIR3* plasmid. In no case did increased levels of *SIR3* restore telomeric silencing.

20

Mutations in *SIR1* do not relieve silencing at telomeres, suggesting that *SIR1* is not involved in controlling TPE (Example II). Consistent with this idea, *SIR3*-overexpression in *sir1⁻* strains enhanced TPE
25 spreading, as observed in wild-type strains. Since the *SIR3* dosage-dependent enhancement of TPE cannot suppress the requirements for *SIR2*, *SIR4*, *NAT1*, *ARD1*, and histone H4, it appears that the *SIR3*-effect operates through the normal mechanism of telomeric silencing, rather than
30 introducing a novel mechanism of silencing.

5. Silenced Chromosomal Domains Spread Continuously from the Telomere

35 The results presented above suggest that the silenced telomeric domain spreads inward along the chromosome in a continuous fashion. To further test this

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idea, two genes were placed adjacent to one another near the same telomere, and the transcriptional state of the centromere-proximal gene was examined when the telomere-proximal gene was transcriptionally active. If the
5 silenced domain is indeed spread continuously along the chromosome, then the centromere-proximal gene should always be derepressed when the telomere-proximal gene is active. However, if the repressed domain is discontinuous, then the centromere-proximal gene may be
10 in a repressed state even when the telomere-proximal gene is active.

Both the *URA3* and *HIS3* genes were inserted near the V-R telomere without a Y' element present; each of the
15 eight possible permutations of *URA3* and *HIS3* located near the V-R telomere was constructed. In addition, three strains were created in which *URA3* and *HIS3* were located on two different chromosomes (V-R and VII-L), either with both genes adjacent to a telomere (UCC2590), or *URA3* at a
20 telomere and *HIS3* non-telomeric (UCC2589), or the converse situation (UCC2591). In order to improve the sensitivity of the spreading assay, the promoters of *URA3* and *HIS3* were weakened by deleting *PPR1* and *GCN4*, the genes which encode their respective transactivators, in
25 each strain. All strains grew in the absence of histidine, indicating that *HIS3* was capable of being expressed at each chromosomal position, although expression was compromised at some telomeric locations (e.g. UCC2577, colony size was small and plating
30 efficiency was reduced on "-his"). All strains carrying a telomeric *URA3* gave rise to colonies which grew on fully-supplemented 5-FOA medium, reflecting transcriptional repression of *URA3*.

35 In the four strains with both *URA3* and *HIS3* located near the V-R telomere, and *HIS3* as the telomere-proximal marker (UCC2576-2579), no growth was detected on "FOA-

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his" medium. That is, when *HIS3* was nearer to the telomere and transcriptionally active, *URA3* was never transcriptionally repressed. In contrast, when *URA3* was telomere-proximal (UCC2580-2583) colonies were obtained on FOA-his, indicating that it was possible for *URA3* to be repressed while *HIS3* was active. Thus TPE spreads continuously inward from the telomere. These results also suggest that the spread of silencing can be blocked by transcription of an intervening gene.

10

Of the four strains with *URA3* in the telomere-proximal location, UCC2581 showed conspicuously poor growth on FOA-his. In this strain, the *URA3* and *HIS3* promoters are separated by only ~0.5 kbp. In such close proximity it might be difficult to open the *HIS3* chromatin structure without also disrupting the silencing apparatus over *URA3*. Another notable result was observed when *URA3* and *HIS3* were located at different telomeres (UCC2590); robust colonies grew on "FOA-his", indicating repression at one telomeric locus while the other telomeric marker was expressed. This result indicates that telomeric silencing is locus-specific.

inventors then examined whether the increased spread of silencing mediated by *SIR3*-overexpression was also continuous. *TRP1* and *URA3* were inserted ~12.5 and 22 kbp, respectively, from the VII-L telomere. 5-FOA^R colonies were observed only when the cells were transformed with YEpsIR3; however, no 5-FOA^R was detected if *TRP1* was simultaneously expressed in these cells. *TRP1* expression by itself was only modestly impaired in YEpsIR3-transformants, as demonstrated by their high efficiency of plating on "-trp-leu". Similar results were obtained when *ADE2* (inserted ~9 kbp from the same telomere) replaced *TRP1* in this study. Taken together, these observations suggest that *SIR3* propagates silencing continuously from the telomere.

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C. DISCUSSION

The inventors have carried out a systematic characterization of the spreading of telomeric position effect (TPE) in *Saccharomyces cerevisiae*. The telomeric position effect in yeast can be considered as a gradient of transcriptional silencing along the chromosome. The inventors postulate that this gradient reflects the limited assembly of a silent chromatin (heterochromatic-like) structure that initiates at the telomere and proceeds continuously inward along the chromosome. In the inventors' analysis, the fraction of 5-FOA^R cells provided an estimate of the frequency at which a telomeric *URA3* was located within this repressive structure.

Transcriptional inactivation of a telomeric locus may be viewed as the final product of a reaction in which subunits of silent chromatin are assembled. In a simple model, silencing of a *URA3* gene six kbp from the telomere would require six times as many subunits than that needed to silence a *URA3* gene located one kbp away. If the assembly of telomeric repressive chromatin were a first-order reaction, then the occurrence of a repressed *URA3* gene at one kbp from the telomere would be expected six times as frequently as when *URA3* is six kbp away. This Example shows that this is not the case. An exponential function more aptly describes the relationship between frequency of silencing and distance from the telomere. Rather the data suggest that telomeric silencing results from the cooperative assembly of subunits, and/or assembly of multiple components. A multimeric representation of silent chromatin is expected to involve the four core histones plus additional components (Eissenberg, 1989; Henikoff, 1990; Spradling and Karpen, 1990; Grigliatti, 1991), as quantitated *in vivo* in this Example.

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It has been proposed that specific terminator sequences along the chromosome act as barriers to heterochromatic spreading (Tartof et al., 1984). No such regions were detected on the telomere-proximal 16 kbp of V-R, nor over 20 kbp of a modified VII-L, although these data do not rule out the existence of such sites in yeast.

Cells carrying *URA3* and *HIS3* located near the V-R telomere, with *HIS3* telomere-proximal, were unable to form colonies on FOA-his media. Since this medium selects for cells in which both *URA3* is repressed and *HIS3* is active, this result demonstrates that silent telomeric domains are continuously propagated from the end of the chromosome in yeast. Since a telomeric gene can be induced to become active Example I, the inventors suggest that transcription may actively block silent chromatin propagation. Alternatively, transcription may not act as a barrier to the spread of silencing *per se*, but rather reflect that the silent telomeric domain assembled only a short distance from the telomere, thus never encompassing the *HIS3* (or *URA3*) gene. The distinction between these two models should be considered in thinking about gene regulation within chromosomal domains.

1. The Role of the Promoter in TPE Spreading

The presence of silent chromatin structures over a telomeric locus appears to impede the access of sequence-specific DNA-binding proteins to the DNA within, thereby generating a TPE (Examples I and II; Gottschling, 1992). These data show a steady decrease in the frequency of silencing compared to the distance of the *URA3* promoter from the telomere. This result strongly suggests that a gene's promoter is a major determinant in *cis* for effective transcriptional repression near telomeres.

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Combined with the finding that silencing of *URA3* does not appear to be dependent on the transcriptional orientation of *URA3*, the inventors propose that repression is primarily exerted on the gene's promoter, and therefore
5 blocks initiation rather than elongation.

Two important points about position effect are provided by the studies in which *PPR1* was deleted. As with most transactivator proteins, *PPR1* appears to
10 modulate transcription through the promoter (Roy et al., 1990). Hence, the increased frequency of telomeric silencing of *URA3* in *ppr1*⁻ strains supports the result that promoter occlusion is critical in achieving position effect repression. These results also suggest that
15 spreading of position effect is a function of promoter strength of the gene being assayed.

A position effect on timing of replication has been detected at ~35 kbp from the V-R telomere (Ferguson
20 et al., 1991; Ferguson and Fangman, 1992), while position effect on *URA3* transcription is not detected beyond ~13 kbp from the same terminus. At present the inventors cannot resolve whether this apparent discrepancy reflects differences between the two assays being used, or
25 inherent distinctions between the mechanisms of initiating replication and transcription.

2. Effect of Y' Elements on the Spread of Telomeric Silencing

30

It has been suggested that Y' elements overcome telomere position effect (Greider, 1992), since genes embedded into Y's are not transcriptionally repressed (Carlson et al., 1985; Louis and Haber, 1990). However,
35 these data argue that Y's do not block the spread of telomeric repression *per se*; the inventors find that a 6.7 kbp Y' element sustains a greater frequency of

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silencing than an equal length of unique chromosomal sequences. It is unclear whether Y's are involved in propagation or reinitiation of silencing, or if Y's simply lack elements present in unique chromosomal DNA which suppress the spreading of telomere-dependent transcriptional inactivation. Nevertheless, the presence of a Y' element adjacent to a telomere results in a more extensive silent chromosomal domain. Perhaps this trait is important in maintaining the unique telomeric presence of Y' elements.

3. *SIR3* Enhances Position Effect in Yeast

Overexpression of *SIR3* enhances position-effect variegation of telomeric genes; this *SIR3*-effect was also detected within and adjacent to the *HM* loci. Thus the modulation by *SIR3* of position-effect repression is likely to occur at other places in the genome where an initiation site for *SIR3*-dependent silencing resides.

The slope of the observed gradient in frequency of *URA3* silencing along V-R is altered by overexpressing *SIR3* in the cell, suggesting that, in contrast to the effect of a *ppr1* mutation, *SIR3*-overexpression affects silent chromatin rather than an intrinsic property of *URA3*. In addition, the increase in telomeric silencing is sensitive to *SIR3* gene dosage, indicating that *SIR3* is limiting in the cell. These data suggest that *SIR3* may be a structural component of yeast repressive chromatin, or a factor directly required for its assembly. Alternatively, *SIR3* may act indirectly by regulating the level or activity of structural or assembly constituents of silent chromosomal domains.

SIR3 bears no significant similarity to any known enhancers of position effects, such as the *Drosophila* Su(var)2-5 (HP-1) or Su(var)3-7 proteins (Alberts and

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Sternglanz, 1990), nor does it harbor a detectable chromodomain motif, which is thought to mediate the packaging of heterochromatin by the *Su(var)2-5* and *Polycomb* gene products (Paro and Hogness, 1991; Messmer et al., 1992). Extragenic suppressor analysis of *HML* silencing indicates a physical interaction between SIR3 and histone H4 (Johnson et al., 1990). Thus the inventors favor the model that SIR3 directly interacts with yeast nucleosomes to facilitate the compaction of chromatin into a higher-order structure responsible for silenced regions of the yeast genome. In this light, SIR3 may be a functional equivalent of histone H1, mediating supranucleosomal organization of the genome (Weintraub, 1984).

15

In addition to histone H4, telomeric silencing requires the products of *SIR2*, *SIR4*, *NAT1* and *ARD1*. The roles of SIR2 and SIR4 in transcriptional repression are not yet clear. NAT1 and ARD1, which are subunits of an N-terminal acetyltransferase (Park and Szostak, 1992), presumably modify chromatin component(s) to facilitate assembly of repressed chromosomal states (Mullen et al., 1989; Park et al., 1992).

25

The ability of telomeric silencing to spread along the chromosome raises the question as to whether a cell can control the size of silenced domains. This issue is particularly critical for *S. cerevisiae*, in which inappropriate regional silencing might have immediate deleterious effects, due to the high density of genes along the chromosome (Olson, 1991). A *cis*-element can act as a chromosome-specific barrier against the spread of silent domains [e.g. active transcription units (this work), or homologues of the *Drosophila scs* sequences (Kellum and Schedl, 1992)]. On a cellular scale, limiting the amount of SIR3 in the cell could prevent excessive transcriptional inactivation of the entire

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genome. Since the *SIR3* gene is itself located near a telomere (Ivy et al., 1985), and no essential gene has been found between *SIR3* and the telomere (Basson et al., 1987; Brisco et al., 1987; Dietzel and Kurjan, 1987; Mortimer et al., 1992), position-effect repression of the *SIR3* locus would provide a plausible negative feedback mechanism for control of position-effect spreading in yeast. If telomeric chromatin spread as far as the *SIR3* locus, transcription of *SIR3* would be repressed, thus limiting further spreading of the repressive chromatin. In apparent contrast to the yeast genome, larger eukaryotic genomes are extensively heterochromatic. This may be due to the presence of more abundant functional homologue(s) of *SIR3*. Extensive but carefully controlled heterochromatization of chromosomes may play a major role in control of cellular differentiation and development in complex eukaryotes.

This Example shows that the spread of telomeric position effect in *S. cerevisiae* is modulated by numerous factors, including promoter distance from the telomere, promoter strength, transcriptional status of telomere-proximal genes, presence of Y' elements, and intracellular concentration of the *SIR3* gene product.

25

EXAMPLE IV

A Transactivator Competes to

Establish Gene Expression in a Cell Cycle Dependent Way

In multicellular eukaryotes, chromosomal position effects generally involve the repression of a euchromatic, wild-type gene when it has been placed in or near heterochromatin as the result of a chromosomal rearrangement (Lima-de-Faria, 1983). In a population of cells with such a rearrangement, the gene may escape repression; consequently, the resulting phenotype is variegated, exhibiting patches of normal and mutant

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tissue. A classic example of this phenomenon is the mosaic red-and-white eye of *Drosophila* in which the white gene has been translocated within centromeric heterochromatin (Eissenberg, 1989; Henikoff, 1990; Spradling and Karpen, 1990).

When a wild-type gene is located near a telomere in the budding yeast *Saccharomyces cerevisiae*, it too is subject to position-effect variegation (Example I). For instance, when yeast cells with the *ADE2* gene placed near a telomere form a colony on solid medium, the colony is composed of sub-populations in which the *ADE2* gene is either expressed (white sectors) or repressed (red sectors). The different phenotypes of the sectors in a colony reflect the ability of genetically identical cells to switch between phenotypic states. The fact that large sectors are phenotypically uniform reflects the ability of each state to be heritably propagated for multiple generations.

20

Similarly, yeast cells with a telomeric *URA3* gene can form colonies on medium containing 5-FOA, a drug lethal to cells expressing *URA3* (Boeke et al., 1987), indicating that the cells are phenotypically *ura3⁻*. However, these 5-FOA resistant cells can form colonies when placed on medium lacking uracil, thus the cells are able to switch their phenotypic status and induce expression of the telomeric *URA3* gene (Example I).

Silencing of telomeric genes in *S. cerevisiae* is likely due to a structurally distinct chromatin domain that initiates at the telomere. Evidence for this specialized chromatin structure includes: identification of mutations in the histone H3 and H4 genes which relieve telomeric silencing (Example II) the finding that telomere-adjacent chromatin contains histone H4 in a hypoacetylated state compared to H4 in actively

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transcribed chromatin regions of the genome (Braunstein et al., 1993), and the relative inaccessibility of telomere-proximal DNA to *in vivo* modification by the *E. coli* dam methyltransferase protein (Gottschling, 1992).

5

In addition, the frequency with which a gene is silenced decreases with increasing distance from the telomere, suggesting that the structure nucleates at the telomere and the extent of its inward assembly along the chromosome varies between cells (Example III; Renauld et al., 1993). The extent of this assembly is proportional to the cellular concentration of SIR3, a gene product required for silencing at telomeres and the silent mating loci, *HML* and *HMR* (Example II; Laurenson and Rine, 1992; Example III). These results suggest that SIR3 is rate-limiting for assembly of the silent chromatin structure, and implicate SIR3 as a component of the silent structure.

20 Questions that arise in the study of position effect variegation are how does a gene switch between phenotypic states and, once a state is determined, how is it heritably propagated (Brown, 1984; Weintraub, 1985). With respect to position-effect variegation and the first question, two models of regulation that involve a role for chromatin structure have evolved (Felsenfeld, 1992). Both models propose that transcription of a gene is inhibited by assembly of its DNA into chromatin. Furthermore, one or more transcriptional activator proteins (transactivators) bind in a sequence-specific manner to DNA located in proximity to the gene and facilitate transcription of that gene, thus overcoming the chromatin's repressive nature. Where the models differ is that in one case chromatin prevents the transactivator from gaining access to the DNA, in essence keeping the gene 'irreversibly' repressed. However, during DNA replication the chromatin structure of the

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gene is perturbed and the transactivator has the opportunity to gain access and establish transcription, before re-assembly of the chromatin is completed. In the second case, the transactivator can induce gene transcription at anytime in a replication-independent manner, effectively disrupting the repressive nature of the chromatin.

At its normal locus, *URA3*, like many biosynthetic pathway genes, is constitutively expressed at a basal level, but can be induced to higher levels of expression (Lacroute, 1968). *URA3* induction is contingent upon binding of an activated form of the transactivator PPR1 to the Upstream Activating Sequence (UAS) of the gene (Losson and Lacroute, 1981; Roy et al., 1990). Interestingly, when *URA3* is located adjacent to a telomere its basal level of expression may be repressed, since the cells are phenotypically *ura3⁻* (Example I).

This Example concerns how a gene located near a telomere overcomes silencing. Specifically, the inventors examined the role of PPR1 in the expression of a telomeric *URA3* gene. The results show that silent telomeric chromatin inhibits basal expression of *URA3* and prevents the transcriptional activation by PPR1 of the telomeric *URA3* gene in G_1 and early S phases of the cell cycle, in addition to when cells are arrested in G_0 . Furthermore, this suggests that upon replication of the telomeric DNA, a competition takes place between assembly of a silent chromatin structure and assembly of a PPR1-mediated transcriptionally active gene.

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A. METHODS

1. Plasmid Constructions

5 Plasmid FAT-PPR1 was constructed by ligating a 4.4 kbp *EcoRI* fragment containing the *PPR1* gene (from pUC8-PPR1, obtained from R. Losson) into plasmid YE

FAT10 (referred to as "FAT"; 2 μ ARS, *TRP1*, *leu2-d*, obtained from K. Runge; Runge and Zakian, 1989). A 3.7 kbp
10 *HindIII*-*SphI* fragment containing the entire *PPR1*-1 allele (from plasmid pFL11; Losson and Lacroute, 1983) was inserted into plasmid pVZ1 (Henikoff and Eghtedarzadeh, 1987). The resulting plasmid (pVZPPR1-1) provided a 3.7 kbp *HindIII*-*BamHI* fragment containing *PPR1*-1 which was
15 ligated into pRS425 (Sikorski and Hieter, 1989) to yield plasmid pRS4-PPR1-1.

Plasmids pRS305-GALPPR1-1 and pRS305-GALppr1-1 were constructed in a series of steps. A 685 bp *EcoRI*-*BamHI*
20 fragment containing the *GAL1*,10 promoter (Johnston and Davis, 1984, from pBM150) was ligated into *EcoRI*-*BamHI* digested pRS314 (Sikorski and Hieter, 1989), the resulting plasmid (pRS314GAL) was digested with *ApaI*-*EcoRI* and a 2.8 kbp *ApaI*-*EcoRI* fragment containing the 3'
25 portion of *PPR1*-1 from plasmid pRS4-PPR1-1 was inserted yielding pRS3GAL3'PPR1-1. Next, a 500 bp fragment containing the 5' portion of the *PPR1*-1 allele was produced by PCR amplification (Innis et al., 1990). The primers were designed to introduce an *EcoRI* site 28 bp
30 upstream of the *PPR1* ATG initiation codon and to include the *EcoRI* site within the *PPR1*-1 coding sequence (*PPR1*-ATG oligo, 5'-CCGGAATTCATACGAAGATGATGATTAAATC-3', SEQ ID NO:6, the new *EcoRI* site is underlined; *PPR1*-n650 oligo, 5'-GGCTTGCCATAGACTTGCTCG-3', SEQ ID NO:7). The fragment
35 was digested with *EcoRI* and inserted between the *GAL1*,10 promoter and the 3' *PPR1*-1 sequence in pRS3GAL3'PPR1-1; one orientation of the insert yielded pGALPPR1-1 which

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has the *GAL1,10* promoter fused to the entire *PPR1-1* coding sequence (*GALPPR1-1*), while the other orientation of the insert yielded *pGALppr1-1* which has the 5' portion of the *PPR1-1* allele inverted resulting in a mutated gene fusion (*GALppr1-1*). The 3.5 kbp *ApaI-BamHI* fragments containing *GALPPR1-1* and *GALppr1-1* from *pGALPPR1-1* and *pGALppr1-1* respectively, were inserted into *pRS305* (Sikorski and Hieter, 1989) yielding *pRS305-GALPPR1-1* and *pRS305-GALppr1-1*.

10

Plasmid *pVZADH4* contains the *ADH4* locus on a 3.1 kbp *EcoRI-SalI* fragment (Example I). A 4.8 kbp *HindIII-XbaI* fragment containing the *LYS2* gene from plasmid *pDP6* (Fleig et al., 1986) was inserted into *XbaI-HindIII* digested *pVZADH4* creating *pVZadh4::LYS2*. The *UAS_{GAL}-URA3* allele was produced by sequential PCR amplification steps (Ausubel et al., 1989). The primers were designed to replace the *PPR1* binding site (*UAS_{URA}*, 5'-TTCGGTAATCTCCGAA-3', SEQ ID NO:8 (Roy et al., 1990)) with a *GAL4* binding site (*URA3-GAL-5'* oligo, 5'-CGGACGACTGTCGTCCGTCAAAAAAATTTCAAGGAAACCG, SEQ ID NO:9, *URA3-GAL-3'* oligo, 5'-CGGACGACAGTCGTCCGCAGAAGGAAGAACGAAGGAA, SEQ ID NO:10, the *GAL4* binding sequence is underlined (Verdier, 1990)).

25

The *UAS_{GAL}-URA3* PCR product was digested with *SalI* and *BamHI* and inserted into *pRS315(-PstI)* producing *pRS315(-PstI)-GALURA3*; the *PstI* site in *pRS315* was previously deleted by digestion of *pRS315* (Sikorski and Hieter, 1989) with *PstI*, making the ends blunt with T4 DNA polymerase, and religating the plasmid. Plasmid *pRS315(-PstI)-GALURA3* was digested with *HindIII* and *SmaI* and religated, resulting in the *UAS_{GAL}-URA3* fragment being inverted in the vector to yield *pRS315(-PstI)-GALURA3-flip*.

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This plasmid provided a 1.1 kbp *HindIII*-*Bam*HI fragment containing *UAS_{GAL}*-*URA3* which was inserted into pVII-L *URA3*-TEL (Example I) to produce pADH4*GALURA3*TEL; the same 1.1 kbp *HindIII*-*Bam*HI *UAS_{GAL}*-*URA3* fragment was
5 inserted into *HindIII*-*Bam*HI digested pVZADH4 resulting in plasmid pΔ*adh4::GALURA3*. A 1.2 kbp *HindIII*-*Not*I fragment (made blunt-ended with T4 DNA polymerase, from pVII-L *URA3*-TEL) was ligated into *HindIII* (made blunt ended with T4 DNA polymerase) digested pVZ*adh4::LYS2* producing
10 p*URA3*-TEL-*LYS2*. A 1.5 kbp *Pst*I fragment (from pADH4*GALURA3*TEL) containing the *UAS_{GAL}*-*URA3* promoter was inserted into *Pst*I digested p*URA3*-TEL-*LYS2* to replace the wild-type *URA3* promoter; the resulting plasmid was
p*GALURA3*-TEL-*LYS2*.

15

A 1.35 kbp *Bam*HI fragment containing the entire *URA1* gene (Roy, 1992) produced by PCR amplification of genomic DNA (5' *URA1* oligo, 5'-CGAACGGATCCCCTTCAGCCACTACAGCCTACTT-3', SEQ ID NO:11; 3' *URA1* oligo, 5'-
20 CGAAGGGATCCGCCAATTGCGAATGCACTCACCG-3', SEQ ID NO:12, the *Bam*HI sites are underlined) was inserted into pVZ1 to yield plasmid pVZ*URA1*. A 1.1 kbp *HindIII*-*Bam*HI *URA3* fragment was ligated into *HindIII*-*Bam*HI digested plasmid YDpK (Berben et al., 1991), yielding plasmid YDpK-*URA3*.
25 Plasmid p5' *URA3* contains a 415 bp *HindIII*-*Eco*RV 5' *URA3* fragment ligated into *HindIII*-*Eco*RV digested pVZ1. Plasmid CY807+*TRP1* (*bar1::TRP1*) was constructed by inserting a 723 bp *Bam*HI fragment containing *TRP1*, from YDp-W (Berben et al., 1991), into the *Bgl*II site in the
30 *BAR1* sequence in plasmid CY807 (obtained from S. Honigberg).

Plasmids pBM292 (*GAL4*-wild-type, 881 amino acids), pBM430 (*GAL4*, C-term. amino acid 292), pBM433 (*GAL4*, C-term. amino acid 684), pBM789 (*GAL4*, C-term. amino acid
35 174), and pBM1268 (*GAL4*, C-term. amino acid 383) are *CEN*, *TRP1* plasmids, as described by Johnston (1988). Plasmids

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pBD57 and pJM206 were obtained from F. Cross, and plasmid pPL9 was obtained from R. Surosky (1992).

2. Yeast Methods and Strains

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S. cerevisiae were grown at 30°C; liquid cultures were agitated during incubation at 180 RPM. All studies in liquid culture were carried out with mid-log phase cells unless otherwise indicated. Plating efficiency analysis and synthetic media have been described previously (Example I), except for α -aminoadipate containing medium which was prepared as described in (Sikorski and Boeke, 1991). Studies involving galactose control employed YEP-3% raffinose, and 0.3% galactose for induction unless otherwise indicated.

15

For studies involving drug or α -factor washout, cells were pelleted by centrifugation for three minutes at 1500 x g and washed and/or resuspended in prewarmed medium (30°C). Cells were arrested with 20nM α -factor for three hours, and 50mM phthalic acid (pH=5.5) was included in the medium. For release from α -factor arrest, 1 mg/ml pronase E was included in the fresh resuspension media, except for one study where one water wash of the pellet was carried out and pronase E was not included in the resuspension medium. Cells were arrested with 10 μ g/ml nocodazole (from a 1000x stock solution in DMSO) for three hours. Hydroxyurea was dissolved directly in medium immediately before use to a final concentration of 400 mM, except in one study where it was dissolved directly in the cultures. Cells were fixed and stored in 10 mM Tris, 100 mM EDTA, pH=8.0, 3.7% formaldehyde, and sonicated before microscopy to assess cell morphology.

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S. cerevisiae were transformed using the lithium acetate procedure (Ito et al., 1983). The *URA3* gene was placed adjacent to the telomere sequence (TG₁₋₃)_n on the

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left end of chromosome VII (UCC2013), or inserted at the *ADH4* locus about 20 kbp from the telomere on VII-L (UCC432), as described in Example I. UCC2013 was derived from YPH499, UCC432 was derived from UCC431.

5

Strains UCC111, UCC113, UCC115, UCC412, and UCC2014 were constructed by transformation of strains UCC1001, UCC1003, YPH250, UCC411, and UCC2013 respectively, with plasmid pΔPPR1::HIS3 and selection for HIS⁺ transformants; this plasmid was described in Example III. Strains UCC116, UCC117, and UCC151 were derived from strains UCC1001, UCC1003, and YPH250 respectively, by transformation with plasmid pFAT-PPR1 and selection for TRP⁺ cells; strains UCC238, UCC152, and UCC153 were derived from strains UCC1001, UCC1003, and YPH250 respectively, by transformation with plasmid YEpfAT10 (FAT) and selection for TRP⁺.

Strain UCC411 was derived from YPH499 by transformation with *HpaI* digested YDpK-URA3 and selection for LYS⁺ cells. UCC413 and UCC2016 were derived from UCC412 and UCC2014 respectively, by transformation with plasmid CY807+TRP1 digested with *ClaI*. Strain UCC431 was a 5-FOA^R (*ura*⁻, *lys*⁻) derivative of UCC413. Strains UCC409, UCC433, and UCC435 were derived from strains UCC2016, UCC431, and UCC432 respectively, by transformation with *HpaI* digested pRS305-GALPPR1-1; strains UCC410, UCC434, and UCC436 were derived from strains UCC2016, UCC431, and UCC432 respectively, by transformation with *HpaI* digested pRS305-GALppr1-1.

In order to place *UAS*_{GAL}-URA3 (or another non-selectable marker) adjacent to telomere VII-L, a method was developed based on the phenomenon of new telomere formation at internal telomeric sequences (Example I). Plasmid pGALURA3-TEL-LYS2 was used to integrate within the *ADH4* locus: *UAS*_{GAL}-URA3 adjacent to

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81 bp of telomere repeat sequence followed by *LYS2* as the selectable marker (centromere-proximal to centromere-distal). At a frequency of $\sim 10^{-6}$, loss of chromosomal sequences distal to the 81 bp internal telomeric sequence (including *LYS2*) resulted in formation of a new and stable telomere having the *UAS_{GAL}-URA3* gene adjacent to it.

Cells that were transformed with pGALURA3-TEL-LYS2, and were *LYS*⁺ and had the correct sequences inserted within the *ADH4* locus (verified by DNA blot hybridization analysis), were grown non-selectively for about 25 generations. Cells which had lost *LYS2* were selected for survival on medium containing α -aminoadipate; the expected structure of telomere VII-L in the resulting *lys*⁻ strain was verified by DNA hybridization analysis.

UCC418 was derived from YM725 by transformation with *NotI-SalI* digested plasmid pGALURA3-TEL-LYS2 and selection for *LYS*⁺ transformants; UCC420 was an α -aminoadipate resistant (*lys*⁻) derivative of UCC418 which has *UAS_{GAL}-URA3* adjacent to telomere VII-L. UCC419 was derived from YM725 by transformation with *EcoRI-SalI* digested plasmid pDadh4::GALURA3 and selection for *URA*⁺ transformants. Strains UCC419 and UCC420 were transformed with plasmids pBM292, pBM430, pBM433, pBM789, and pBM1268, to yield strains UCC421-UCC425 respectively, for the UCC419 parent, and strains UCC426-UCC430 respectively for the UCC420 parent. The expected structures of the various chromosomal constructs were confirmed by DNA blot hybridization analysis.

3. Analysis of Nucleic Acids

RNA was isolated from mid-log phase cells, unless otherwise indicated, as described in Example I. RNA hybridization analyses were performed as described in

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Example I, except that 15 or 20 μ g of total RNA was denatured in the presence of 20 μ g/ml ethidium bromide and separated by electrophoresis on a 1.2% agarose-5% formaldehyde (37% stock)-MOPS gel. Immediately following electrophoresis the gel was photographed and washed twice for 15 minutes in H_2O , 15 minutes in 10x SSC and transferred to nylon (MSI, Westboro, MA). Photography of the gel following transfer verified that complete transfer of the rRNA had occurred.

10

RNA was immobilized on the nylon membrane by UV irradiation (120 mJ) of the damp membrane, followed by prehybridization of the membrane. Prehybridization and hybridization solutions contained 5x SSC, 50% formamide, 5x Denhardt's solution, 0.2 mg/ml denatured and degraded herring sperm DNA, 0.2% SDS; hybridization solution also contained 10% dextran sulfate and was filtered through a 45 μ m membrane to remove particulates. Prehybridization (1-6 hr) and hybridization (18-30 hr) were carried out at 42°C for DNA probes and 53°C for RNA probes.

20

Blots were washed five minutes at 23°C in 2x SSC, 0.1% SDS, followed by two 15 minutes washes at 55°C in 0.1x SSC, 0.1% SDS for DNA probes, or three 20 minute washes at 60°C in 0.1x SSC, 0.1% SDS for RNA probes, and exposed to film. The relative levels of *URA3* and *URA1* RNAs were quantified on a Radioanalytic Imaging System (Ambis, San Diego, CA). For rehybridization studies, probes were removed from the blots with three 20 minute washes with boiling 0.2% SDS.

30

RNA antisense probes were labeled with ^{32}P -CTP or ^{32}P -UTP (3000 Ci/mmol) by *in vitro* transcription of linearized plasmids with T7 RNA polymerase or SP6 RNA polymerase (Sambrook et al., 1989). DNA probes were labeled with ^{32}P -dCTP (3000 Ci/mmol) by random oligonucleotide priming as described (Sambrook et al.,

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1989). Plasmid p5'URA3 (T7) was the template for the URA3 RNA probe. Plasmid pPL9 (SP6) was the template for the ACT1 RNA probe. The URA3 DNA probe was a 1.1 kbp HindIII fragment containing the entire coding sequence, the URA1 probe was a 1.3 kbp BamHI fragment containing the entire URA1 gene in plasmid pVZURA1, the SWI5 probe was a 3.3 kbp HindIII fragment from pBD57, and the CLN2 probe was a 640 bp HindIII-SpeI fragment in pJM206.

10 B. RESULTS

1. The URA3 Transactivator, PPR1, Is Required for Overcoming Telomeric Silencing of URA3

15 In order to test the idea that the transactivator, PPR1, plays a role in overcoming silencing of a telomere-linked URA3 gene, the PPR1 gene was deleted from a strain in which URA3 was located adjacent to telomere VII-L (UCC1001). To determine whether deletion of PPR1 had a specific effect on URA3 expression at a telomere, PPR1 was also deleted in a strain with URA3 inserted at an internal chromosomal position, the ADH4 locus which is about 20 kbp from telomere VII-L (UCC1003). PPR1 was also deleted in a strain lacking URA3 (ura3-52; YPH250).

25

URA3 expression was measured by two methods: plating viability assays on medium containing 5-fluoro-orotic acid (5-FOA) and on medium lacking uracil (-URA), and RNA blot hybridization analysis. 5-FOA is converted into a toxic metabolite by the URA3 gene product, such that cells expressing normal levels of the URA3 gene product are sensitive to 5-FOA, while cells that lack it are resistant to 5-FOA (Boeke et al., 1984).

35

For the RNA analysis, transcript levels were analyzed from URA3, URA1, and ura3-52 (Rose and Winston, 1984, in this allele the URA3 transcript is truncated)

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each of which is regulated by the PPR1 protein (Losson and Lacroute, 1981). Thus, *URA1* and *ura3-52* RNA levels reflect the *in vivo* level of PPR1 activity as a transcriptional activator in each experimental sample.

5

PPR1 was found to be required for overcoming silencing of the telomeric *URA3* gene. Wild type (*PPR1*⁺) cells with *URA3* near a telomere, formed colonies on 5-FOA medium and medium lacking uracil. This reflects the ability of the telomeric *URA3* gene to switch between transcriptionally repressed and active states. Deletion of *PPR1* abolished the ability of cells with a telomeric *URA3* gene to grow in the absence of uracil. Deletion of the PPR1 binding site within the *URA3* gene promoter had the same effect as deletion of *PPR1*, indicating that specific binding of PPR1 at the *URA3* UAS was required for overcoming silencing. Thus, in this telomeric context, PPR1 is required for the transcriptional activation of the *URA3* gene.

20

The very small colonies which arose on -URA medium from the *ppr1*⁻ strain with a telomeric *URA3* gene had acquired *trans*-acting mutations or local chromosomal rearrangements which permitted expression of *URA3*. Therefore, essentially no *URA3* gene product was produced from this telomeric site when PPR1 was absent from the cell. In contrast, deletion of *PPR1* had no effect on 5-FOA or -URA viability when *URA3* was located at an internal chromosomal locus. This result suggests that at an internal location transcription of *URA3* still occurs, independently of PPR1, and is consistent with *URA3* regulation at its normal chromosomal locus (Losson et al., 1985). As expected, *PPR1* deletion had no effect on the plating viability of cells lacking a functional *URA3* gene.

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Telomeric *URA3* mRNA was undetectable when *PPR1* was deleted. However, *PPR1*⁺ cells with a telomeric *URA3* maintained the ability to activate *URA3* transcription. Deletion of *PPR1* had little or no effect on expression of
5 an internal copy of *URA3*, or on expression of *URA1*.

Both the plating viability on -URA medium and the RNA analysis indicate that the constitutive or basal (PPR1-independent) expression of *URA3* at telomere VII-L
10 is repressed by the telomeric silencing machinery. However, the transactivator, *PPR1*, is able to circumvent the telomeric repression, thus facilitating *URA3* expression.

15 **2. Increased PPR1 Dosage Prevents Silencing of a Telomeric *URA3***

Since a telomeric *URA3* could exist in either an active or repressed state, and because *PPR1* was required
20 for the active state, the inventors postulated that *PPR1* might compete against the assembly of a repressed state. If this hypothesis were true, then increasing the dosage of *PPR1* should increase the frequency with which an active state is established.

25

To test this hypothesis, *PPR1* was expressed from a multi-copy plasmid (FAT-*PPR1*, FAT is the vector alone) in strains with *URA3* absent, *URA3* at a telomeric, or *URA3* at an internal chromosomal locus. Cell viability of the
30 resulting strains was quantified on 5-FOA medium and medium lacking uracil. Increase of *PPR1* protein concentration from FAT-*PPR1* (verified by *ura3-52* and *URA1* RNA levels and quantitative electrophoretic mobility shift analyses) resulted in complete 5-FOA-sensitivity of
35 cells with *URA3* at the telomeric locus, along with improved growth on -URA. As expected, viability was not affected by overproduction of *PPR1* when *URA3* was at the

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internal locus or absent. Thus, high levels of PPR1 compete against telomeric silencing to perpetually maintain the *URA3* gene in an active state. These results also suggest that in a wild type cell, the concentration of PPR1 is limiting for telomeric *URA3* expression.

3. GAL4 Can Overcome Telomeric Silencing

To determine if the ability of PPR1 to overcome telomeric silencing on *URA3* transcription was a general characteristic of transcriptional activator proteins, the PPR1 binding site upstream of the *URA3* gene was replaced with a binding site for the GAL4 transactivator protein (Verdier, 1990). This modified *URA3* gene (*UAS_{GAL}-URA3*) was placed next to telomere VII-L (UCC420) or within the *ADH4* locus (UCC419) in strain YM725 (*gal4⁻*, *gal80⁻*, *ura3⁻*). The *gal80* mutation relieves negative regulation of the GAL4 protein so that activity of GAL4 is proportional to its concentration (Johnston, 1987). *UAS_{GAL}-URA3* was silenced when placed at telomere VII-L, as the cells were 5-FOA-resistant and *Ura⁻*, but *UAS_{GAL}-URA3* was not repressed when internally located on the chromosome since cells were 5-FOA-sensitive and *URA⁺*.

The wild-type GAL4 protein or a series of C-terminal truncations of the GAL4 protein were expressed in the strains with *UAS_{GAL}-URA3* located at the telomere or at the internal locus. The C-terminal truncation derivatives of GAL4 maintain the N-terminal DNA binding domain and bind to *UAS_{GAL}* *in vitro*, but are defective in transcriptional activation *in vivo* (Johnston and Dover, 1988). Expression of wild-type GAL4, from a single copy centromeric plasmid, completely reversed silencing of the telomeric *UAS_{GAL}-URA3*, as indicated by the sensitivity of this strain to 5-FOA, and robust growth on -URA medium. None of the truncated GAL4 derivatives were able to activate *UAS_{GAL}-URA3* adjacent to the telomere. Expression

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of GAL4 or its derivatives had no effect on 5-FOA-sensitivity, or -URA viability, of strains with *UAS_{GAL}-URA3* located internal on the chromosome. It appears that the activation domain of GAL4 is required to compete for
5 telomeric gene expression. These results suggest that the ability to overcome telomeric silencing is a general function of transactivators.

10 4. Modulating the Dosage of PPR1^c Reveals that Its
 Accessibility to the Telomeric *URA3* Gene is
 Limited

15 The finding that PPR1 dosage has a demonstrable effect on telomeric *URA3* expression, but not for internal *URA3* expression, suggested that the telomeric *URA3* gene is relatively resistant to transcriptional activation by PPR1 compared to when *URA3* gene is located non-telomerically.

20 To investigate this, a chimeric gene, *GALPPR1-1*, was constructed with the coding sequence of the *PPR1-1* allele under control of the *GAL1,10* promoter (Johnston and Davis, 1984). The *PPR1-1* allele encodes a constitutively active protein, PPR1^c; thus, the level of PPR1^c activity
25 as a transactivator is directly proportional to its total cellular concentration (Losson and Lacroute, 1983). The *GAL1,10* promoter permitted precise regulation of PPR1^c protein concentration within the cell (Durrin et al., 1991), since the intracellular level of PPR1^c was
30 proportional to the level of galactose in the medium (based on *ura3-52* RNA levels and quantitative electrophoretic mobility-shift analyses). As a control, a non-functional version of the gene fusion (*GALppr1-1*), which contains an inversion within the *PPR1-1* coding
35 sequence, was also created. These gene fusions were inserted at the *leu2* locus in isogenic *ppr1*⁻ strains containing *URA3* at a telomeric (UCC2016) or internal

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chromosomal locus (UCC431) or in which *URA3* was absent (UCC432).

The resulting strains were tested for viability on 5-FOA and -URA medium that also contain galactose. Expression of the *GALPPR1-1* fusion, but not the mutated *GALppr1-1* fusion, effectively overcame silencing of the telomeric *URA3* in all cells of the population; the cells were *URA*⁺ and 5-FOA-sensitive. Expression of *GALPPR1-1* or *GALppr1-1* had no effect on the 5-FOA sensitivity or the -URA viability of strains with *URA3* at the internal locus or absent.

Levels of mRNA were analyzed from these strains grown in rich medium containing 3% raffinose and 0.25% galactose, which induced expression of *GALPPR1-1* or *GALppr1-1*. Expression of *GALPPR1-1* strongly activated transcription from *URA3*, *URA1*, and *ura3-52*, although compared to expression of the internal *URA3* gene, expression of the telomeric *URA3* was reduced. Equivalent levels of PPR1^C activity [based on *URA1* and *ura3-52* mRNA levels, and electrophoretic mobility-shift analyses] were present in the *GALPPR1-1* strains. This result supports the idea that, compared to the internal *URA3*, the telomeric *URA3* gene is relatively resistant to transcriptional activation at this concentration of PPR1^C.

The inventors compared the relative expression levels of the telomeric *URA3* gene and the internal *URA3* gene when different concentrations of PPR1^C protein were expressed. The level of *ura3-52* RNA was used as a standard for PPR1^C concentration *in vivo* in comparing the two *URA3* loci; *ura3-52* has the same upstream sequences as *URA3* and is responsive over a wide range of PPR1^C concentrations. The level of *GALPPR1-1* expression was varied by growing cells with different concentrations of

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galactose in the medium; levels of *ura3-52* RNA confirmed that higher concentrations of galactose did in fact result in higher intracellular PPR1^c protein concentrations.

5

The results show that *URA3* at the telomeric locus was less responsive to low levels of the transactivator than *URA3* at an internal locus. In addition, while both loci can achieve the same maximum level of expression, a higher PPR1^c concentration was required for the telomeric *URA3* compared to the internal *URA3*. These results suggest that there is a competition for binding at the telomeric *URA3* promoter between PPR1^c and silent chromatin.

15

5. PPR1^c Activation of a Telomeric *URA3* Gene Is Cell Cycle Regulated

The studies described above were performed on actively dividing cells. Hence, the cells were transiting through the cell cycle during the analysis. Keeping this in mind, two simple models can be set forth to explain the competition between PPR1 and telomeric chromatin for expression of the *URA3* gene. In the first model, the competition only occurs within specific periods of the cell cycle. During part of the cell cycle the telomeric *URA3* gene is resistant to activation by PPR1 if the silent chromatin state has been established. Only when the silent chromatin is weakened or disassembled, which might occur during DNA replication of the telomeric region, does PPR1 have the opportunity to activate the gene. In the second model, PPR1 competes with equal fervor throughout the cell cycle.

35

To test and distinguish between these models, cells were grown in rich medium containing 3% raffinose and no galactose. Thus PPR1^c was not present and the telomeric

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URA3 gene was maintained in a silent state. The cells were then synchronously arrested by treatment with either α -factor pheromone, to arrest them late in G_1 (Pringle and Hartwell, 1981), or nocodazole, an inhibitor of microtubule assembly (Pillus and Solomon, 1986).

In many eukaryotes, nocodazole produces a synchronous arrest at metaphase. Nocodazole also produces a very synchronous arrest in yeast, however it is unclear whether the arrest occurs late in G_2 or at metaphase. By the criterion of spindle pole body separation the cells appear to be in G_2 (Jacobs et al., 1988); however recent studies suggest that the chromosomes may be condensed as expected for a metaphase arrest (Guacci et al., 1994). In light of this uncertainty, the arrest is referred to as G_2 /metaphase. Once arrested, galactose was added to induce expression of *PPR1-1*, and half of the culture was released from the arrest, while arrest was maintained in the other half.

Expression of the telomeric *URA3* gene and the internal *URA1* and *ura3-52* genes was compared. The transcript levels of *CLN2* and *SWI5* were also analyzed to monitor the progress of cells through the cell cycle. *CLN2* is transiently expressed in late G_1 near the time of START (Wittenberg et al., 1990), and *SWI5* is transiently expressed beginning sometime in S, through G_2 , and on into M (Nasmyth et al., 1987).

The telomeric *URA3* was not activated by *PPR1^c* during α -factor arrest. The analysis clearly shows that while cells were arrested with α -factor, the telomeric *URA3* gene remained repressed. The increase in *URA1* and *ura3-52* mRNA levels indicate that *PPR1^c* was active in these cells. Following release from the α -factor arrest, *PPR1^c* was able to activate the telomeric *URA3* gene. The analysis of the *SWI5* transcript and microscopic analysis

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of cell morphology were consistent with the cell-cycle arrest imposed by α -factor, and release thereafter. The low level of telomeric *URA3* transcript seen late during the continued α -factor arrest correlated with the small
5 fraction of cells (~5%) that escaped from the arrest.

In striking contrast to the repressed state of telomeric *URA3* during α -factor arrest, the telomeric *URA3* gene in G_2 /metaphase, nocodazole arrested, cells was
10 effectively activated by PPR1^C. In the absence of functional PPR1^C, "*GALppr1-1*"), no activation of the telomeric *URA3* or the internal *URA1* and *ura3-52* genes occurred. In fact, not even basal expression of the telomeric *URA3* was seen in the absence of PPR1^C.
15 Analyses of *CLN2* and *SWI5* expression, as well as microscopic analyses of cell morphology, confirmed the successful arrest with nocodazole and the release that followed.

20 To determine whether the effects of the α -factor and nocodazole treatments were due to the specific cell cycle arrests and not to other physiological effects of the treatments, the inventors tested the effect of α -factor on telomeric gene expression in cells arrested in G_2 with
25 nocodazole, and conversely, the effect of nocodazole on telomeric gene expression in cells arrested in G_1 with α -factor.

The α -factor treatment did not prevent the
30 expression of the telomeric *URA3* gene in cells previously arrested with nocodazole, and nocodazole treatment did not result in expression of the telomeric gene in cells previously arrested with α -factor. Thus, it appears that the effects on telomeric gene transcription by α -factor
35 and nocodazole were due to the specific cell cycle arrests. These results suggest that the ability of a transactivator (PPR1^C) to function in a telomeric domain

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is cell cycle regulated. The inventors propose that a transactivator is inaccessible to the telomeric domain in G₁ phase and becomes accessible by the time the cells are in G₂/metaphase.

5

To more accurately determine the period of the cell cycle in which PPR1^C activation of a telomeric *URA3* could occur, cells were arrested in S phase with hydroxyurea, an inhibitor of DNA replication (Slater, 1973). Yeast
10 cells with a telomeric *URA3* and the integrated *GALPPR1-1* fusion were pregrown in medium lacking galactose, to maintain repression of the telomeric *URA3* gene, and arrested with α -factor. Galactose was added to the α -factor arrested cells to induce expression of *PPR1-1*,
15 and the cells were released from the α -factor arrest; half of the culture was released into medium containing hydroxyurea.

Cells treated with this α -factor/hydroxyurea
20 protocol arrest very early in S phase, significantly before telomeric regions replicate (Hartwell, 1976; McCarroll and Fangman, 1988). Hydroxyurea prevented the activation of the telomeric *URA3*, but did not affect transcriptional activation of the internal *URA1* and *ura3-*
25 52 genes. Telomeric *URA3* and *SWI5* expression following release from the hydroxyurea arrest, indicated that the arrest was reversible. Additionally, hydroxyurea did not prevent activation of the telomeric *URA3* gene in cells which were previously arrested in G₂/metaphase with
30 nocodazole, indicating that the presence of hydroxyurea itself does not prevent telomeric *URA3* expression. These results indicate that early in S phase the transactivator can not gain access to the telomeric *URA3*, and taken together with the results above, suggest that progression
35 through S phase is required for the establishment of the transcriptionally active state in the telomeric domain.

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Temperature sensitive alleles of *CDC* (Cell Division Control) genes represent another method commonly used to arrest yeast cells at a specific point in the cell cycle (Pringle and Hartwell, 1981). Cells are typically shifted from a permissive growth temperature (~23°) to a non-permissive temperature (37°) to cause arrest. The inventors began to use temperature sensitive alleles of *CDC* genes to define the cell cycle period in which PPR1 activation occurred. However, it was discovered that PPR1^C-induced expression of a telomeric *URA3* was severely compromised at 37° in wild type (*CDC*⁺) cells (Aparicio, 1993). This finding precluded the use of temperature sensitive alleles in dissecting the period of activation in the cell cycle. The effect appeared to be telomere specific, since the *ura3-52* locus was activated. It is not clear if the effect of temperature on telomeric *URA3* activation was specific to PPR1^C (e.g. a reduction in the effective concentration of PPR1^C), or reflects a general strengthening of telomeric repression.

6. Telomeric Silencing Is Irreversible When Cells Are in Stationary Phase (*G*₀)

An additional means to synchronously arrest a population of yeast cells is to maintain a culture in stationary phase (Werner-Washburne et al., 1993, for a review). Stationary phase cells of *S. cerevisiae* arrest in a state referred to as *G*₀; the cells are unbudded and their genomes are unreplicated. Cells enter *G*₀ by exiting from *G*₁ phase, and general transcriptional repression occurs upon entry to stationary phase (Choder, 1991).

Strains with *URA3* at a telomeric or a nontelomeric locus and an integrated *GALPPR1-1* were grown to stationary phase in rich medium containing 3% raffinose, so that PPR1^C was absent and hence the telomeric *URA3*

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gene was silenced. Cells were determined to be in stationary phase when the optical density of the culture had not increased during the previous 24 hour period, and greater than 98% of cells were unbudded. Expression of
5 GALPPR1-1 was induced in the stationary cells by adding 0.3% galactose to the cultures. Incubation was continued as aliquots were collected for RNA analysis.

While the internal *URA3* gene, as well as the *URA1*
10 and *ura3-52* genes were transcriptionally activated by PPR1^c in the stationary cells, the telomeric *URA3* gene was not activated. Only after 48 hours of induction was a telomeric *URA3* transcript observed, just slightly above limits of detection. Thus, silencing of a telomeric gene
15 in stationary phase cells is essentially irreversible. As expected, basal levels of transcription decreased in the stationary cells. Moreover, the *SWI5* transcript was not detected in G₀ cells, confirming that cells were not progressing through the mitotic cell cycle. In this
20 study, galactose was added to cultures about 48 hours after mid-log phase; equivalent results were obtained when the study was performed with seven day old cultures.

C. DISCUSSION

25

In this Example, the inventors examined the ability of transactivator proteins to overcome silencing of a telomere-adjacent gene in *S. cerevisiae*. It was found that the transactivator protein, PPR1, is absolutely
30 required for expression of a *URA3* gene located immediately adjacent to the left telomere of chromosome VII. In contrast, when *URA3* is at a non-telomeric location, PPR1 merely provides a modest increase in expression (Roy et al., 1990). Two conclusions may be
35 drawn from these results: telomeres inhibit basal transcription, and transactivators have a mechanism to circumvent this inhibition.

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It is likely that the basal transcription apparatus of *URA3* is prevented from accessing the gene's promoter due to steric occlusion by silent telomeric chromatin. This is supported by the observation that other DNA
5 binding proteins, such as *E. coli* dam methylase, are excluded from telomere-proximal DNA regions *in vivo* (Gottschling, 1992). Note that basal expression of *URA3*, as with most housekeeping genes in yeast, requires not only a TATA element but additional sequences upstream
10 that bind PPR1-independent factors (Roy et al., 1990).

These results show that, first, PPR1 cannot activate transcription of the telomeric *URA3* gene in G_1 , early S, or G_0 cells. Only in a G_2 /metaphase arrest is activation
15 observed. Second, the cellular concentration of PPR1 dramatically affects the frequency with which telomeric *URA3* expression is established. Third, the complete activation domain of a transactivator is essential for its efficacy. While a telomeric gene with a GAL4 UAS can
20 be activated in the presence of wild type GAL4, the gene remains silenced when the wild type GAL4 is replaced by derivatives which remove the GAL4 transcriptional activation domain.

25 The inventors propose a replication-dependent model to explain how a telomeric gene can overcome silencing to become transcriptionally active. In G_1 of the cell cycle, a silenced telomeric gene is packaged in a repressive chromatin structure which is relatively
30 "static" and prevents interactions of the DNA with other DNA binding proteins such as basal transcription factors and transactivators. However, the telomeric chromatin loses its static structure, as a result of the DNA replication process or some other coordinate cellular
35 event. Alternatively, one of the two newly replicated sister chromatids retains the silent chromatin while the

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other is essentially 'naked' DNA and awaits assembly into chromatin.

Regardless of which pathway occurs, upon completion
5 of replication, two distinct assembly processes compete
to establish the transcriptional state of a telomeric
gene. Assembly of silent chromatin initiates at the
telomere and propagates inward along the DNA. This
10 process requires not only the histones but a number of
additional factors, such as RAP1, SIR2, SIR3, and SIR4
(Example II; Kyrion et al., 1993). The competing process
involves the binding of the transactivator protein to the
telomeric gene and assembly of an active transcription
15 complex. The competition ends when one of the two
processes is fully established at the promoter region of
the telomeric gene. In the absence of competition from
the transactivator, the silent chromatin eventually
assembles into its static structure. The moment that
20 this silent structure forms, defines the end of the cell
cycle period in which the transactivator has an
opportunity to compete.

Having a limited period in the cell cycle during
which a transcriptional state is established has several
25 ramifications. Environmental or genetic changes that
alter the length of the silent chromatin assembly process
could dramatically affect the frequency of establishing a
state. Such changes may be direct. For instance, the
SIR3 gene product appears to be a component of silent
30 chromatin that is rate-limiting in its assembly (Johnson
et al., 1990; Example III). Thus increasing SIR3
concentration increases the frequency of establishing
repression (Example III). Alternatively, changes that
extend periods of the cell cycle in which silent
35 chromatin assembly occurs, such as G_2 , provide a
transactivator greater opportunity to establish an active
state. Conversely, a shorter G_2 would favor

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establishment of a silent state. In essence, such changes can dictate the amount of phenotypic variegation within a population of cells.

5 The assembly of silent telomeric chromatin may consist of several distinct, sequential steps rather than an 'all-or-none', concerted process. In nocodazole-arrested cells, telomeric *URA3* expression was rapid when PPR1 was present (*GALPPR1*). However, basal, or PPR1-
10 independent (*GALppr1*), expression of the telomeric *URA3* was not detected, even after a lengthy arrest (~5 hr); while basal expression at internal loci was normal. These results suggest that at the nocodazole-arrest point silent chromatin is assembled up to a stage that
15 precludes basal expression, yet does not prevent PPR1-induced expression.

 This postulated intermediate of silent chromatin assembly may not be locked into a fully static structure,
20 yet it is still more recalcitrant to gene expression than other areas of the genome. The static chromatin structure likely requires several contributions: binding of the core histones by accessory proteins such as SIR3 (Example III) modifications of telomeric histones such as
25 hypoacetylation (Braunstein et al., 1993), and localization of the structure to the nuclear periphery (Palladino et al., 1993). Any of these contributions may be absent at an intermediate stage.

30 These results extend observations made at the yeast silent mating type loci, *HML* and *HMR* (Miller and Nasmyth, 1984). Telomeres and the *HM* loci share a number of silencing factors (e.g. SIR2, SIR3, and SIR4) and Nasmyth determined, using temperature sensitive alleles of *SIR3*
35 and *SIR4*, that establishment of silencing at the *HM* loci requires passage through S phase, and thus presumably DNA replication. Their conclusion is consistent with the

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model the inventors propose, that the competition for assembly occurs after replication. Furthermore, the inventors show that, at least in the case of the VII-L telomeric locus, assembly of silencing is not completed until sometime after G₂/metaphase (nocodazole-arrest).

Miller and Nasmyth also found that inactivating the *SIR3* or *SIR4* gene product at any time in the cell cycle resulted in gene expression at the *HM* loci. Here, the inventors show that passage through S phase is required for activation of a telomeric gene. Thus, dismantling of the repressive chromatin, either by artificially compromising it with a defective *SIR3* or *SIR4* allele, or in every cell cycle during passage through S phase, allows a renewal of the competition between establishment of active and silent states.

As the result of a telomeric location, *URA3* can be much more highly regulated than at its normal locus. When *URA3* is at a non-telomeric location, the presence of PPR1^C produces a three to seven-fold induction over basal expression (Liljelund et al., 1984). However, with *URA3* near a telomere, an equivalent amount of PPR1 induces expression about 100-fold. The inventors suggest that the genomes may have evolved to take advantage of this type of telomeric regulation. For example, *Trypanosomes* depend upon the highly regulated expression of the telomeric VSG (Variable Surface Glycoprotein) genes (Borst, 1991, Cross, 1990).

When cells were in G₀, essentially no amount of transactivator protein was sufficient to overcome telomeric silencing, while at an internal non-silenced position the transactivator readily induced expression. Interestingly, general transcriptional repression, apparently mediated by chromatin changes, occurs upon entry to stationary phase (Choder, 1991). In fact,

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stationary phase chromosomes display different sedimentation properties than G_1 phase chromosomes, suggesting that chromosomes assume a distinct compact structure in G_0 cells (Piñon, 1978). It is possible that
5 the same machinery and mechanism of telomeric silencing in G_1 extends to other regions of the genome in G_0 , thus facilitating the more global compaction and transcriptional repression.

10 Whatever the nature of the silent telomeric chromatin, it contrasts with the chromatin structure of the *PHO5* gene in yeast. While this locus is transcriptionally repressed by nucleosomes upstream of the transcription initiation site, it can be induced
15 rapidly at anytime in the cell cycle or in G_0 arrested cells (Schmid et al., 1992). The induction involves the displacement of a nucleosome by the gene's transcriptional activator protein. In contrast, overcoming telomeric silencing requires that the
20 nucleosomes be modified or removed by passage through S phase before the transactivator protein can have its effect. This emphasizes that telomeric chromatin is inherently different than chromatin at *PHO5* or most other regions of the yeast genome.

25

EXAMPLE V

Identification of Genes that Suppress Telomeric Silencing

Genes located near *S. cerevisiae* telomeres are
30 subject to transcriptional silencing by a repressive chromatin structure that initiates at the telomeres (Gottschling et al., 1990; Gottschling, 1992; Renauld et al., 1993; Examples I through IV). The inventors hypothesized that the telomeric structure responsible for
35 silencing is likely to be a multimeric complex that would be sensitive to the stoichiometric imbalance of its components. Therefore, in order to identify genes

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involved in telomere structure or function, the inventors carried out a screen for gene products that, when expressed at high levels, would suppress telomeric silencing.

5

A yeast strain was constructed with genetic markers located at two telomeric loci. The *ADE2* gene, which is required for adenine biosynthesis, was placed adjacent to the telomere at the right arm of chromosome V (V-R), and
10 *URA3*, a gene required for uracil biosynthesis, was located adjacent to the telomere at the left arm of chromosome VII (VII-L).

More specifically, the strain used for
15 transformation with the library was UCC3505 (*MATa ura3-52 lys2-801 ade2-101 trp1-Δ63, his3-Δ200 leu2-Δ1 ppr1::HIS3 adh4::URA3-TEL DIA5-1*). *DIA5-1* refers to the directed integration of *ADE2* adjacent to telomere V-R. UCC3505 was constructed by successively transforming YPH499
20 (Sikorski & Hieter, 1989) with pVII-L *URA3-TEL* (Gottschling et al., 1990), pΔPPR1-*HIS3* (Renauld et al., 1993), and pHR10-6. Plasmid pHR10-6, obtained from H. Renauld, was constructed by inserting a 2.8 kb Hind III fragment from plasmid pV-R *URA3-TEL* (Gottschling et al.,
25 1990), containing sequences from the subtelomeric region of chromosome arm V-R, into the Hind III site of pYTCA-2 (Gottschling et al., 1990), such that the Eco RI site of the insert was furthest from the Bam HI site of the vector, thus creating pHR9-9. Into the Bam HI site of
30 pHR9-9 was inserted the 3.4 kb Eco RI-Bam HI fragment containing the *ADE2* gene from pL909 (Gottschling et al., 1990), thus creating pHR10-6. The *ADE2* gene is oriented with its promoter proximal to the V-R sequences. pHR10-6 was cleaved with Eco RI for use in fragment-mediated
35 transformation of yeast.

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Normally, colonies expressing *ADE2* are white, while those not expressing it (*ade2*) are red (Roman, 1956). Due to the semi-stable nature of telomeric silencing of most genes, switching between silenced and transcriptionally active states may occur every few generations, giving rise to different phenotypic populations. In the case of strains with *ADE2* near a telomere, these different populations are seen as red and white sectors within a single colony (Gottschling et al., 1990). A *URA3* gene located at telomere VII-L also normally switches between transcriptional states (Gottschling et al., 1990). However, the telomeric *URA3* was caused to be completely silenced by deleting its trans-activator, *PPR1* (Aparicio & Gottschling, 1994). The cells were therefore unable to grow in the absence of uracil.

To identify genes or gene fragments whose overexpression could disrupt silencing, the strain was transformed with a high-expression *S. cerevisiae* cDNA library. The pTRP plasmid expression library used in this study was created with *cre-lox* site-directed recombination from the λ TRP library (obtained from S. J. Elledge, Baylor College of Medicine, Houston). The pTRP vector contains a 2 μ origin of replication and the *TRP1* selectable marker. The cDNA inserts were cloned into a Xho I site of the pTRP vector, placing them under the control of the *GAL1* promoter. The creation of similar libraries is described in Elledge et al. (1991).

By the nature of its synthesis, a cDNA library typically contains both full length and truncated versions of RNA transcripts. Thus high level expression from a cDNA library has two means of causing a stoichiometric imbalance: by expression of a normal gene product or a defective one (Herskowitz, 1987). In the library used in this study, the expression of cDNA

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inserts was controlled by the *GAL1* promoter, which is strongly induced by the presence of galactose in the medium (Johnston & Davis, 1984). Of the 330,000 yeast transformants obtained, 48 displayed a galactose-dependent decrease in telomeric silencing. That is, when grown on media containing galactose, the cells were able to grow in the absence of uracil (*Ura*⁺) and gave rise to predominantly white colonies (*Ade*⁺). On the basis of restriction mapping, DNA blotting (Southern) analysis, and DNA sequencing, it was determined that these 48 clones represented ten independent genes.

EXAMPLE VI

Isolation of *TLC1*, a Telomere-Specific Suppressor of Silencing

The genes known to be required for telomeric silencing are also involved in transcriptional silencing at two internal chromosomal sites, the *HML* and *HMR* loci, which harbor the unexpressed copies of the mating type genes in *S. cerevisiae* (Aparicio et al., 1991). To determine whether the newly isolated suppressors of telomeric silencing also affect silencing at *HML*, the expression plasmids were introduced into a strain in which the *URA3* gene was inserted into the *HML* locus. The strain used for assaying silencing at the *HML* locus was UCC3515 (*MAT α lys2-801 ade2-101 trp1- Δ 63 his3- Δ 200 leu2- Δ 1 ura3-52 hml::URA3*). The *hml::URA3* construct is the same as that described for strain GJY5 (Mahoney & Broach, 1989). Overexpression of one of the novel genes identified, *TLC1*, had no effect on silencing at *HML*, but strongly suppressed telomeric silencing of *URA3* and *ADE2* (FIG. 1A, FIG. 1B and FIG. 1C). The *SIR4* gene, whose overexpression disrupts silencing both at telomeres and at *HML* (Marshall et al., 1987), was also isolated in the present screen and derepressed both of these loci in this assay (FIG. 1A, FIG. 1B and FIG. 1C).

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Further evidence for the specific association of *TLC1* with telomere structure came from examination of telomere length in strains overexpressing a *TLC1* cDNA clone. In the absence of the *TLC1* overexpression
5 plasmid, the telomeric sequences at VII-L averaged 330 base pairs (bp) in length. Upon overexpression of *TLC1*, the average telomere length at VII-L decreased between 90 and 220 bp (FIG. 2). The alteration of telomere length upon overexpression of *TLC1*, together with the loss of
10 telomeric silencing, suggested that this gene is specifically involved in telomere structure.

Of the 48 cDNA clones isolated in the present screen as suppressors of telomeric silencing, nine represented
15 *TLC1*. The inventors sequenced one of the *TLC1* cDNA clones in its entirety (pTRP61, 1248 bp), as well as the ends of the other eight *TLC1* clones. These sequence data overlapped to yield a contiguous sequence of 1301 bp, although no single clone included the entire sequence.
20 The combined sequence of the *TLC1* cDNA clones has been submitted to GenBank and assigned the accession number U14595.

The span of each of the cDNA clones with respect to
25 the entire 1301 bp fragment is as follows: pTRP6 (1-1248), pTRP61 (54-1301), pTRP14 and pTRP47 (54-1263), pTRP33 and pTRP39 (54-1269), pTRP55 (54-1264 or 1265), pTRP59 (39-1250), pTRP60 (270-1264 or 1265), and pTRP61 (54-1301). Four of the *TLC1* cDNA sequences (in clones
30 pTRP55, pTRP60, pTRP33 and pTRP39) are followed by short stretches (5-20 nts) of adenines. It is not yet clear whether these adenines reflect authentic *in vivo* polyadenylation of the *TLC1* transcripts, or are by-products of cDNA synthesis.

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For reference, both the *TLC1* gene and the RNA template include the CACCACACCCACACAC (SEQ ID NO:3)

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template sequence that ultimately allows the GTGTGTGGGTGTG sequence (SEQ ID NO:2) to be inserted into the telomere. The *TLC1* gene sequence CACCACACCCACACAC (SEQ ID NO:3) spans the region 468-483 of SEQ ID NO:1.

5 In the complementary strand, SEQ ID NO:4, this region is 819-834.

Physical mapping localized *TLC1* to a single site on chromosome II, immediately adjacent to *CSG2*. *TLC1* was mapped by hybridizing the labeled cDNA clone (1.25 kb Xho I insert from pTRP6) to a filter grid containing λ phage clones representing over 96 percent of the yeast genome. The filter set was obtained from the American Type Culture Collection (Olson et al., 1986; Link & Olson,

10 1991; Beeler et al., 1994). Subsequent to the present work, the sequence of chromosome II was entered into the EMBL database. The chromosome II-R sequences have the EMBL accession number X76078. These data matched the present sequence obtained from the cDNAs.

20

RNA blot (Northern) analysis confirmed that a wild-type strain contained a relatively abundant RNA that hybridized to a *TLC1* probe and was approximately 1.3 kilobases (kb) in length (FIG. 3A and FIG. 3B).

25

EXAMPLE VII

TLC1 Encodes the Telomerase RNA

The *TLC1* sequence has two notable features. The gene is unlikely to encode a protein since it does not contain a large open reading frame (ORF). The longest ORF that begins with an ATG codon is only 43 amino acids in length. This finding suggested that the functional *TLC1* gene product might be the RNA itself. Moreover,

30 *TLC1* contains the sequence CACCACACCCACACAC (SEQ ID NO:3), which includes the motif predicted to template *S. cerevisiae* telomeres (Kramer & Haber, 1993). These

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results suggested to the inventors that *TLC1* encodes the putative yeast telomerase RNA.

To confirm that the *TLC1* gene product is indeed the telomerase RNA, the *TLC1* gene was disrupted. The inventors predicted that this would cause incomplete replication of telomeres and result in progressive telomere shortening with each cell division. A *TLC1* gene disruption was created in which a large part of *TLC1*, including the predicted telomere-templating region, was removed and replaced with a marker gene.

For the gene disruption, the *TLC1* cDNA clone in plasmid pTRP61 was excised away from pTRP vector sequences as a 1.25 kb *Xho* I fragment, and inserted into the *Xho* I site of pBluescript II KS(-) (Stratagene; La Jolla, CA), creating pBlue61. The disruption of *TLC1* was created by replacing the 693 bp *Nco* I-*Nsi* I fragment of pBlue61 with a blunt-ended *Bam* HI 1.6 kb *LEU2* clone from plasmid YDp-L (Berben et al., 1991), creating pBlue61::LEU2. This construct was digested with *Xho* I and transformed into the diploid strain UCC3507, selecting for *Leu*⁺ transformants, to produce UCC3508 (UCC3507 *TLC1/tlc1::LEU2*). Southern blot analysis confirmed that UCC3508 was heterozygous for the disruption at the *TLC1* locus.

Nineteen out of nineteen tetrads sporulated from UCC3508 yielded 2:2 segregation of the *tlc1::LEU2* allele. The genotype of UCC3507 is: *MATa/MATa ura3-52/ura3-52 lys2-801/lys2-801 ade2-101/ade2-101 his3-Δ200/his3-Δ200 trp1-Δ1/TRP1 leu2-Δ1/leu2-Δ1 adh4::URA3-TEL/adh4::URA3-TEL DIA5-1/DIA5-1 ppr1::HIS3/ppr1::LYS2*. The haploid strains crossed to create UCC3507 were derived from YPH250 and YPH102 (Sikorski & Hieter, 1989). The introduction of changes into the genotypes of these haploids all utilized plasmids described above, except

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allele *ppr1::LYS2*, which was introduced using plasmid *pAPPR1::LYS2* (Renauld et al., 1993).

5 The disrupted gene was introduced into a wild-type
diploid strain to create a *TLC1/tlc1* heterozygote, which
was then sporulated, giving rise to two mutant and two
wild-type haploid strains. Northern analysis confirmed
that in the *TLC1*-disrupted spore products, there was no
detectable *TLC1* RNA (FIG. 3A and FIG. 3B). The spore
10 colonies were inoculated into rich medium and grown for
several days by diluting the cultures into fresh medium
every 24 hours. In all cases examined (eight tetrads),
TLC1 strains maintained a normal telomere length after 6
days of growth. In contrast, the *tlc1* strains displayed
15 shortened telomeres. In the cases where DNA samples were
collected daily (three tetrads), the *tlc1* telomeres were
found to shorten progressively, at an approximate rate of
3 bp per generation (FIG. 4A).

20 In conjunction with the shortening telomere
phenotype, older *tlc1* cultures displayed a gradual
increase in generation time. Through the first 40
generations after sporulation of a *TLC1/tlc1* strain, all
four spore products were able to regrow approximately one
25 thousand-fold in rich medium within 24 hours, indicating
a generation time of less than 2.4 hours (FIG. 4B). This
growth rate was maintained in *TLC1* strains for up to 80
generations.

30 In contrast, the *tlc1* strains, by 65 generations
after germination, the growth rate had slowed to about
3.3 hours/generation. After 75 generations, the doubling
time of the *tlc1* cultures was 5.7 hours. This decrease
in growth rate was accompanied by a 50 % drop in
35 viability in the *tlc1* strains after 75 generations. This
general pattern was clear in all 14 tetrads examined,
although there was some variation in the period at which

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the decrease in growth rate occurred. However, as was reported for *est1* strains (Lundblad & Blackburn, 1993), the dying *tlc1* cultures were overwhelmed within approximately 100 generations by faster-growing cells, which presumably contained suppressor mutations.

To demonstrate that the *TLC1* gene product was the *S. cerevisiae* telomerase template RNA, it was necessary to confirm that *TLC1* sequences encoded telomeric tract repeats. Earlier studies with *Tetrahymena thermophila* showed that when a mutated telomerase RNA is introduced into a cell, the altered sequence may then be templated into the cell's telomeres (Yu et al., 1990). A candidate motif for the telomere template within *TLC1* was the sequence CACCACACCCACACAC (SEQ ID NO:3) (FIG. 5A). The inventors constructed a *TLC1* allele, designated *TLC1-1(Hae III)*, in which two base pairs of this motif were changed to create a recognition site for the restriction enzyme Hae III (FIG. 5B).

The mutant *TLC1-1(Hae III)* allele was used to replace one of the normal *TLC1* genes in a diploid strain as follows: Plasmid pVZ61b was constructed by inserting the 1.25 kb Xho I fragment containing the *TLC1* cDNA clone from pTRP61 into the Sal I site of plasmid pVZ1 (Henikoff & Eghtedarzadeh, 1987). The *TLC1-1(Hae III)* mutant allele was generated using two oligonucleotides, Hpa I primer (5'-TCCAGAGTTAACGATAAGATAGAC-3') and Hae III primer (5'-TAATTACCAT GGGAAGCCTA CCATCACCAGGCCACACAC AAATG-3'; SEQ ID NO:5 [Greider and Blackburn, 1985, 1987, 1989; Zahler and Prescott, 1988; Morin, 1989; Prowse et al., 1993; Shippen-Lentz and Blackburn, 1989; Mantell and Greider, 1994; de Lange, 1994; Greider, 1994; Harley et al., 1992]) to PCR-amplify a 232-bp fragment from plasmid pVZ61b.

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The PCR product was then cleaved with Nco I and Hpa I, to create a 213 bp fragment that was used to replace the 213-bp Nco I-Hpa I fragment of pBlue61, to create pBlue61-Hae III. The 213 bp fragment was sequenced from the pBlue61 plasmid to verify that the PCR amplification did not introduce additional mutations into the sequence.

The *TLC1-1(Hae III)* allele, contained in a 1.25 kb Xho I fragment, was then cleaved from pBlue61-Hae III and inserted into the Xho I site of pRS306 (Sikorski & Hieter, 1989), to create the integrating plasmid pRS306-*TLC1-1(Hae III)*. This latter construct was digested with Afl II and used to transform YPH501 (Sikorski & Hieter, 1989), with selection for Ura⁺ transformants, thus creating the heterozygous strain UCC3520. UCC3522 (YPH501 *TLC1-1(Hae III)/TLC1*) was isolated as a 5-fluoro-orotic acid-resistant derivative of UCC3520 in which the pRS306-*TLC1* plasmid had recombined out of the *TLC1* locus, which left the *TLC1-1(Hae III)* allele in the chromosome (Scherer & Davis, 1979), as confirmed by Southern blot analysis.

In addition to functioning at the very ends of normal telomeres, telomerase is also believed to play an important role in the healing of broken chromosomes and the extension of unusually short telomeric tracts (Kramer & Haber, 1993). In this latter capacity, the activity of a mutant telomerase would be most easily detected. Therefore, fragment-mediated transformation was used to remove the sequence distal to the *ADH4* locus on the left arm of chromosome VII, and replace it with a *URA3* gene and a short tract of telomeric sequence to act as a seed for in vivo telomere elongation (FIG. 6A).

This transformation was done in both homozygous wild-type (*TLC1/TLC1*) and heterozygous *TLC1-1(Hae III)/TLC1* strains. The *ADH4-URA3-TG₁₋₃* fragment used to

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replace the left arm of chromosome VII was generated by Not I-Sal I digestion of plasmid AD3ARUGT-IV. This plasmid was constructed by the following set of steps: the 1.1 kb Hind III-Sma I DNA fragment containing *URA3* (Rose et al., 1984) was inserted into the Hinc II site of pYTCA-2 by blunt-end ligation, with the promoter of *URA3* proximal to the TG₁₋₃ sequences of the vector, creating plasmid p3ARUCA. The 1.2 kb Hind III fragment of pYA4-2, containing *ADH4* (Lundblad & Szostak, 1989; Williamson & Paquin, 1987), was then inserted into the Hind III site of p3ARUCA, with the Sal I site of the insert distal to the *URA3* gene in the vector, creating plasmid pAD3ARUCA. Finally, the Sal I-EcoR I fragment containing the composite insert (*ADH4-URA3-TG₁₋₃*) from pAD3ARUCA was cloned into pVZ1, creating AD3ARUGT-IV.

The yeast strains that were transformed with the *ADH4-URA3-TG₁₋₃* fragment were YPH501 (*TLC1/TLC1*) and UCC3522 (*TLC1-1(HaeIII)/TLC1*). These studies were repeated with the transforming *ADH4-URA3-TG₁₋₃* DNA liberated from the pAD3ARUGT-IV plasmid as a Sal I-EcoR I fragment, and results similar to those reported in FIG. 6B were obtained.

Southern analysis was performed on genomic DNA from the transformed strains to determine the structure of the new telomeres at VII-L (FIG. 6B). Digestion with Apa I, whose most distal site in the new VII-L arm occurs within the *URA3* gene, demonstrated that in both the wild-type (*TLC1/TLC1*) and heterozygous *TLC1-1(Hae III)/TLC1* transformants, the new chromosomal end was extended in vivo to several hundred base pairs. The new telomeres in the *TLC1-1(Hae III)/TLC1* strain were slightly shorter and more heterogeneous in length than those added in the *TLC1/TLC1* strain.

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In all twelve *TLC1/TLC1* independent transformants tested, digestion with Hae III, which cuts at the same site in *URA3* as Apa I, indicated that no Hae III sites were introduced during telomere elongation *in vivo*. In contrast, in all eight *TLC1-1(Hae III)/TLC1* independent strains examined, Hae III sites were incorporated into the newly formed telomere. It can thus be concluded that the mutated sequence in the *TLC1-1(Hae III)* gene served as a template for the addition of telomeric repeats, which indicates that the *TLC1* gene indeed encodes the *S. cerevisiae* telomerase RNA.

EXAMPLE VIII

TLC1 Compared to Other Telomerase RNAs

In these studies the inventors demonstrated the existence of an *S. cerevisiae* telomerase and identified the gene that encodes its RNA component (Examples V through VII). These above findings support the proposal that the telomerase mechanism of replicating the ends of chromosomes is widespread among eukaryotes. However, the *TLC1* RNA is much larger (1.3 kb) than the known ciliate telomerase RNAs, which are 160 to 200 nucleotides (nt) in length (Blackburn, 1993). This discrepancy in gene size is reminiscent of the 1175 nt *S. cerevisiae* U2 snRNA, which is almost 1 kb larger than the mammalian U2 snRNA (Ares, 1986). The conserved secondary structure that is shared among the ciliate telomerase RNAs is not apparent in the sequences surrounding the *TLC1* template region (Romero & Blackburn, 1991; ten Dam et al., 1991), though the large size of the transcript may allow homologous structures to form that are not obvious at this time. *TLC1* also lacks a short primary sequence adjacent to the template region that is conserved among the ciliate telomerase RNAs (Lingner et al., 1994).

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While telomeric DNA in most organisms is comprised of sequences repeated in a regular fashion, e.g. mammalian (T_2AG_3), *Tetrahymena* (T_2G_4), the telomeric sequence of *S. cerevisiae* is irregular $[(TG)_{1-3}TG_{2-3}]$ (Zakian, 1989). However, this irregularity can be fully explained by the telomere-templating sequence in *TLC1*. Telomerase RNAs are thought to synthesize the G-rich strand of telomeres by multiple rounds of hybridization to a short sequence at the end of a telomeric tract, elongation of the DNA by a limited reverse transcription of the RNA, and disengagement (Blackburn, 1993). In vitro, the *Tetrahymena* telomerase RNA appears to use as few as three nucleotides for the hybridization step (Autexier & Greider, 1994).

The telomere template region of *TLC1* (CACCACACCCACACAC; SEQ ID NO:3) suggests that the telomerase RNA may be able to align with a telomere terminus at a number of different points within the RNA, especially if CAC is all that is required for hybridization. It is also possible that the telomerase could abort a round of reverse-transcription at several different positions along the RNA. If a terminal DNA sequence such as GTG is left, then alignment with the CAC RNA motif in the next round of elongation can readily occur. Either alone or in combination, these different alignment and termination possibilities can account for the heterogeneity observed in the *S. cerevisiae* telomeric tracts.

30

EXAMPLE IX

Telomeric Silencing and Telomerase

Overexpression of the *TLC1* cDNA clones identified in the present studies (Examples V through VIII) both disrupts telomeric silencing and causes a shortening of telomeres. One model to explain these results is that

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overexpression of the cDNAs causes limiting telomerase components to be titrated into incomplete and nonfunctional complexes, thereby reducing the total telomerase activity in the cell and resulting in shorter telomeres. The length of the telomere may relate to its ability to bind silencing proteins; shorter telomeres simply have fewer binding sites, and thus may silence telomeric genes less efficiently (Kyrion et al., 1993). Alternatively, the telomerase RNA itself, or one of the factors it binds, may be an integral component of the complex that is required for silencing at telomeres. Overexpression of *TLC1* may perturb the stoichiometry of this complex, and thus interfere with its assembly. It is noteworthy that of the nine *TLC1* cDNAs isolated in the present screen, none appear to be full length. Thus it is formally possible that only an incomplete (non-functional) *TLC1* RNA can produce the effects detected.

The telomere shortening and growth defects observed when the telomerase RNA was disrupted are very similar to those described for *est1* strains, supporting the prediction that *EST1* is a constituent of telomerase (Lundblad & Szostak, 1989). Moreover, the genetic link discovered here between telomeric silencing and telomerase suggests future approaches for identifying other telomerase components, which so far have been elusive.

EXAMPLE X

Other Genes Identified by Telomeric Silencing

Using the telomeric silencing protocol described herein, the inventors isolated 48 clones. On the basis of restriction mapping, DNA blotting (Southern) analysis, and DNA sequencing, it was determined that these 48 clones represented ten independent genes. Of the these ten genes, four have been sequenced and identified

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previously. These genes are the *SIR4* (Marshall et. al., 1987); *ASF1* (Le and Sternglanz, Genbank Accession Number 107593); *RPL32* (Dabeva and Warner, 1987); and *RRP3* (Cherel and Thuriaux, Genbank Accession Number z29488).

5

The new genes are herein termed *STR* genes, Suppressors of Telomeric Repression. Initially, seven *STR* genes were designated, although *STR7* was later found to correspond to part of the sequence for *RRP3*. *STR2* has
10 been renamed *TLC1* following its functional characterization, as shown in FIG. 7A and FIG. 7B.

The DNA and predicted amino acid sequences, where relevant, of the *STR* genes are as defined in Table 2.

15

TABLE 2

Gene	DNA SEQ ID NO:	Complementary Strand SEQ ID NO:	Polypeptide SEQ ID NO:	Probes & Primers Projected SEQ ID NOS:
<i>STR1</i>	15	29†	16	5837-7702
<i>TLC1 (STR2)</i>	1	4	*	33-1317
<i>STR3</i>	17	30†	18	7703-8780
<i>STR4</i>	19†		20	1318-3735
<i>STR5</i>	21	31†	22	8781-9571
<i>STR6</i>	23†		24	3736-5836
<i>STR7</i>	25	32†	26	
<i>RRP3</i>	27†		28	

20

25

* Encodes RNA Template - SEQ ID NO:3
† Denotes strand with protein-encoding open
30 reading frame

Table 2 shows the DNA and amino acid sequences of seven of the *STR* genes. *STR2*, renamed *TLC1*, encodes the RNA template component, rather than a polypeptide

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species. Both SEQ ID NO:1 and SEQ ID NO:4 are provided for *TLC1*. *STR7* (SEQ ID NO:25, DNA; and SEQ ID NO:26, amino acid) was found to be a partial sequence of *RRP3*, the full length sequences of which are also included
5 herein (SEQ ID NO:27, DNA; and SEQ ID NO:28, amino acid).

Table 2 also provides information concerning the numbers of 17-mer probes and primers from SEQ ID NO:1 and from each of the polypeptide-encoding DNA sequences of
10 the present invention. Naturally, the number of 17-mers from each of the complementary strands could be readily made. Given that 32 separate sequences are already disclosed herein, should the 17-mer probes and primers from the claimed sequences be specifically identified and
15 numbered, they would start with SEQ ID NO:33.

The projected SEQ ID NO designations in Table 2 refer to the individual sequences that could be readily predicted from the given information. For example, the
20 sequence AATAAACTAGAGAGGA, residues 1 to 17 of SEQ ID NO:1, would be assigned SEQ ID NO:33; the sequence ATAAACTAGAGAGGAA, residues 2 to 18 of SEQ ID NO:1, would be assigned SEQ ID NO:34. On this basis, SEQ ID NO:100 would be ATTTTTTTTTTTTTCAG, residues 68 to 84 of SEQ ID
25 NO:1; SEQ ID NO:1000 would be GATCAAGAACGTAATTT, residues 968 to 984 of SEQ ID NO:1; SEQ ID NO:5000 would be AAAAGATGAAGACGCTT, residues 1265 to 1281 of SEQ ID NO:23; and SEQ ID NO:9571 would be AGATATTCTAACTCTCT, residues 791 to 807 of SEQ ID NO:31.

30

The start and stop site locations for the major open reading frames (ORFs) of each of the *STR* sequences are presented in Table 3. The ORFs for *STR4* and *STR6* are presented with respect to the DNA strand originally
35 sequenced. It was noted that certain of the DNA sequences had ORFs oriented in the opposite direction to the original DNA strand sequence, so that the ORF starts

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at a high position in the DNA, and ends at a low position. Namely, the *STR1* ORF was located between nucleotides 1829-84; the *STR3* ORF was located between nucleotides 1017-1; and the *STR5* ORF was located between nucleotides 753-109. Although this phenomenon is well known, the complementary DNA strand of *STR1*, *STR3*, *STR5* and *STR7* are also included herein (SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31 AND SEQ ID NO:32, respectively; Table 2 and Table 3), and the ORFs listed in ascending numbers for instant recognition.

TABLE 3

Gene	Original Strand SEQ ID NO:	Complementary Strand SEQ ID NO:	ORF Starts at (bp #)	ORF Ends at (bp#)	Length of ORF (Amino Acid Residues)
<i>STR1</i>	15	29†	54	1799	582
<i>STR3</i>	17	30†	78	1094	339
<i>STR4</i>	19†		2	2368	789
<i>STR5</i>	21	31†	55	699	215
<i>STR6</i>	23†		3	1955	651
<i>STR7</i>	25	32†	279	956	226

† Denotes strand with open reading frame (ORF)

To determine how strongly each gene suppressed telomeric silencing, viability in the absence of uracil was quantified for the strains that contained the telomeric *URA3* gene and each of the highly expressed genes. All the genes suppressed silencing of the telomeric *URA3*, although a hierarchy of suppression was observed (FIG. 7A).

All previously identified genes known to be required for telomeric silencing are also known to be involved in

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transcriptional silencing at two internal chromosomal sites, the *HML* and *HMR* loci, which harbor the unexpressed copies of the mating type genes in *S. cerevisiae* (Aparicio et al., 1991). To determine whether the newly
5 isolated suppressors of telomeric silencing also affect silencing at *HML*, the expression plasmids were introduced into a strain in which the *URA3* gene was inserted into the *HML* locus (Mahoney & Broach, 1989).

10 Overexpression of the novel gene *TLC1* (*STR2*) had no effect on silencing at *HML*, but strongly suppressed telomeric silencing of *URA3* and *ADE2* (FIG. 7B). The *SIR4* and *ASF1* genes, whose overexpression was previously known to disrupt silencing both at telomeres and at *HML*
15 (Marshall et al., 1987), as well as *STR1*, *STR4*, and *RRP3* genes, derepressed *HML* very well (FIG. 7B). Overexpression of *RPL32*, *STR3*, *STR5* and *STR6* had intermediate effects at *HML* (FIG. 7B).

20

EXAMPLE XI

Detailed Analysis of the *TLC1* Gene and RNA

To define the components of telomerase activity, the telomerase template RNA from *S. cerevisiae* is used in
25 conjunction with classical and molecular genetic techniques to identify the previously elusive telomerase proteins.

Telomere length in *S. cerevisiae* is normally under
30 tight genetic control; telomeres do not grow infinitely long, nor do they become drastically shortened. In addition, a 3' tail is detected at the end of yeast chromosomes late in S-phase. Taken together these observations suggest that telomerase activity is
35 regulated, most likely being limited to late S-phase of the cell cycle. There are numerous mechanisms to explain the proposed modulation of telomerase activity in a cell.

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At a first level of evaluation the models can be divided into those in which (1) the RNA is regulated (the RNA is the limiting component), (2) a different component of telomerase activity (mostly likely a protein) is regulated, or (3) that telomerase activity is constitutive and access to its substrate (the 3' end of the chromosome) is regulated. Validity of these models concerning telomerase regulation is determined as follows.

A. Fine Structure Analysis of the TLC1 RNA

To determine the 5' and 3' ends of the telomerase RNA, standard techniques, such as S1 and ribonuclease protection (for both the 5' and 3' ends), and primer extension (for the 5' end) are used (Sambrook et al., 1989). By using this combination of methods, the physical ends of the RNA are identified.

Typically, non-translated RNAs do not have a polyA⁺ tail. However, of the nine TLC1 cDNA clones isolated in the earlier genetic selection/screen, four had adenine tracts of 5-20 nucleotides at their 3' ends. A recently published method is available for determining the precise sequence of 3' ends of messages, irrespective of whether they have a long, a short or no poly-A tail (Liu & Gorovsky, 1993). The method uses T4 RNA ligase to attach a DNA oligonucleotide to the 3' end of RNA molecules, followed by cDNA synthesis, PCR amplification, cloning and sequencing. This method is capable of detecting a poly-A⁺ transcript if it is represented in only a few percent of the TLC1 RNA population.

The inventors currently believe that the yeast telomerase RNA is not poly-adenylated, but that the subset of TLC1 cDNAs with poly-A tracts that the inventors isolated represent a by-product of the cDNA

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synthesis. However, if the telomerase RNA is polyadenylated in *S. cerevisiae*, it may represent another level of control. For instance, genes involved in poly-A⁺ addition, degradation and message localization
5 have been identified in yeast, and may be important in regulating *TLC1* activity (Muhlrads & Parker, 1992).

B. *TLC1* RNA Expression and Cell-Cycle

10 A simple mechanism for limiting telomerase activity to a specific period of the cell cycle, is to regulate the presence of the telomerase RNA. Therefore the steady-state levels of the *TLC1* RNA through the cell
15 cycle are determined. Methods are available to bring a culture of yeast cells into a synchronized progression through the cell cycle, or to arrest the cells at specific stages (Aparicio & Gottschling, 1994). For instance, *MATa* cells are arrested in late G1 with α -factor or a conditional cell-cycle arrest mutation.
20 Steady state RNA levels are then isolated and analyzed. In addition, the cells are later released from the arrest and allowed to progress synchronously through the cycle, with RNA samples being taken at various times after release. The cell cycle position of the cell population
25 is determined by examining cell morphology and RNA levels of genes known to be cell-cycle regulated (e.g. *CLN2* and *SWI5*). During the analysis of the *TLC1* RNA, any changes in transcript length, particularly if a fraction of the RNA is modified, such as by poly-adenylation, is noted.
30 A cell-cycle change may be the result of cell-cycle regulated transcription or a post-transcriptional event such as RNA degradation.

C. Characterizing the *TLC1* Gene

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The inventors verified that the cDNA clones of *TLC1* isolated are identical to the genomic sequences. Thus,

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it does not appear that any major sequence modifications occur to the telomerase RNA after transcription, such as RNA splicing or editing (Moore et al., 1993; Bass, 1993), although the possibility of post-transcriptional
5 modifications, such as methylation (Reddy & Busch, 1988), cannot presently be ruled out.

The precise positioning of *TLC1* within the genome, and the sequences of the gene's transcriptional control
10 elements, was also determined by the inventors. The 3' ends of *TLC1* and *CSG2* converge from opposite directions. The *CSG2* gene has a predicted ORF that terminates within 50 bp of the 3' end of the *TLC1* cDNA sequences. On the opposite side of *TLC1*, *PDX3* has a divergent transcript
15 with an ORF beginning ~650 bp from the 5' end of the *TLC1* cDNA sequences. Analysis of this intervening 650 bp, particularly in the region within 200bp of the predicted *TLC1* 5' end, reveals matches or very near matches to TATA elements, *GCN4* (Hill et al., 1986) and *HOMOL1* (Rotenberg
20 & Woolford, Jr., 1986) consensus binding sites (both are transcriptional activators that bind to Upstream Activating Sequences (UAS)), and to A block and B block sites (Geiduschek & Tocchini-Valentini, 1988, RNA Polymerase III control elements). Thus at this point,
25 *TLC1* may be transcribed by either Pol II or Pol III.

In order to determine which polymerase transcribes the gene, the steady state level of the *TLC1* message in strains containing a conditional temperature sensitive
30 allele of either Pol II or Pol III is examined, after the cells have been shifted to a non-permissive temperature (Gudenus et al., 1988; Kolodziej & Young, 1991). This analysis, in concert with 5' deletion analysis, allows the RNA polymerase that transcribes the gene to be
35 determined. Sequences for two known cell-cycle specific control elements, an *Mlu* I site or *SWI4/SWI6* consensus binding site (Nasmyth, 1993; Primig et al., 1992), are

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not present upstream of *TLC1*. Thus it is unlikely that *TLC1* transcription is regulated by either of these cell-cycle dependent pathways.

5 The minimum extent of the sequences, both 5' and 3' of *TLC1*, that are required on a single-copy CEN plasmid to complement the chromosomal null mutation *tlc1::LEU2* are determined using, e.g., the plasmid pAZ1 (obtained from Teresa Dunn, Beeler et al., 1994), which contains a
10 5.5 kbp *Sal I* fragment that encodes all of *CSG2* and *TLC1*, and most of *PDX3*. Using restriction enzymes and exonucleases the essential sequences are determined. The reduced size of the gene fragment will greatly facilitate further mutant analysis, and the 5' deletion analysis
15 will determine which UAS-promoter elements are essential for expression, thereby facilitating the creation of a conditional mutant with a heterologous UAS/promoter.

20 **D. Constructing an Allele of *TLC1* that is Regulated by a Heterologous Promoter**

 In order to facilitate *in vivo* studies on *TLC1*, a conditional allele of the gene is useful. A chimeric fusion of the *TLC1* gene placed under the regulation of a
25 heterologous promoter/UAS is contemplated. Based on data from the *TLC1* DNA sequence, the 5' end of the *TLC1* RNA, and determining what sequences at the 5' end of the gene are essential for *TLC1* expression, the *TLC1* upstream region is then replaced with the control elements of the
30 *MET3* gene (Cherest et al., 1987). The *MET3* promoter is repressed in the presence of methionine and induced when methionine is absent from the medium. *MET3* transcriptional fusions to a number of RNA Pol II transcribed genes have been described. The *GAL1,10 UAS*
35 may also be used (Johnston & Davis, 1984). If *TLC1* is transcribed by Pol III, the bacterial tetracycline repressor-operator system may be used to regulate the

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TLCl gene. A Pol III-transcribed gene has been shown to be regulated by this system when the *tetO* operator sequence was introduced near the 5' end of the gene in *S. cerevisiae* (Dingermann et al., 1992).

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The plasmid shuffle technique (Sikorski & Boeke, 1991) and conditional alleles may also be used in place of heterologous promoters.

10

EXAMPLE XII

The Role of *TLCl* in Additional in vivo Processes

A. Telomerase RNA and Single-Strand TG_{1-3} Tails

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A single-strand TG_{1-3} tail at the ends of yeast telomeres is transiently detected late in S phase (Wellinger et al., 1993). This tail may be the result of elongation of the 3' strand at chromosome ends by telomerase activity. Tail formation in a *tlc1* strain (Wellinger et al., 1993) is thus examined. The TG_{1-3} tails are detected by using a Southern hybridization method in which yeast DNA is never denatured, and then hybridized with a $C_{1-3}A$ probe. When the tails are ≥ 65 nucleotides long, the probe efficiently hybridizes to the single-strand of TG_{1-3} . The analysis is performed on cells that are synchronously progressing through S phase after release from an α -factor arrest (late G1), or a *cdc7* arrest (G1-S boundary). In a wild type (*TLCl*) cell the same results as previously observed are expected, but in a *tlc1* strain, no tail detection is contemplated. However, if a single-strand tail is still observed in a *tlc1* strain, then the tail is likely to be formed by a telomerase-independent mechanism. For instance, the tail may be formed by loss of terminal 5' $C_{1-3}A$ strand sequences, the result of a cell-cycle controlled exonuclease activity. The *tlc1* allele used in this study is a conditional allele placed under a heterologous

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promoter. Alternatively, young (< 50 generations old) haploid cells, the spore products of a *TLC1/tlc1* diploid strain, are used.

5 The role of *EST1* in tail formation (Lundblad & Szostak, 1989) is also examined. If tail formation is dependent upon both *TLC1* and *EST1*, it lends support that *EST1* is part of telomerase, or regulates its activity. Alternatively, if the tail is only dependent upon *TLC1*,
10 it suggests that *EST1* may be important in another aspect of telomere replication, perhaps in synthesis of the 5' strand.

B. Telomerase RNA and Healing Broken Chromosome Ends

15 When a chromosome is broken, two non-telomeric DNA ends are generated; these ends are unstable. One mechanism for stabilizing ends is to 'heal' them by the addition of telomeric sequences. Telomerase activity may
20 provide a major mechanistic pathway for healing by adding telomere DNA *de novo* to the broken ends (Kramer & Haber, 1993; Harrington & Greider, 1991). An alternative pathway, which has been documented in *S. cerevisiae* and *Drosophila*, utilizes recombinational mechanisms
25 (Biessmann & Mason, 1992).

 To test telomere healing, a Haber-based assay is used (Kramer & Haber, 1993). In this system, a recognition sequence for the *HO* endonuclease is located
30 at a unique site in the genome of a diploid cell (on only one of the homologues), with markers genes on either side of it. The *HO* endonuclease is then conditionally expressed (it is under control of a galactose-dependent promoter) and results in cleavage of the single
35 homologue. The strain is *rad52⁻*, which eliminates the major mitotic recombination pathway in yeast, thus preventing repair of the broken chromosome by gene

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conversion from the uncut homologue, or telomere healing by the recombination pathway (Lundblad & Blackburn, 1993). By selecting for cells that retain a marker centromere proximal to the cut site, and loss of a marker telomere proximal to the cut, healed chromosomes are identified. A diploid cell is required in this system, because essential genes are lost distal to the cut site; these gene functions are provided by the uncut homologue.

10 The inventors have designed a new genetic system, improved (FIG. 8) in several important ways: (1) The unique *HO* cleavage site is introduced at the *ADH4* locus into a haploid strain. *ADH4* and the sequences distal to it are non-essential for haploid growth; thus, they may be lost without apparent consequence (Gottschling, 1990). The haploid nature of the strain is of particular use in genetic identification and analyses of recessive mutations. (2) A short tract of TG_{1-3} is placed centromere-proximal of the *HO* cleavage site. This sequence serves as a 'seed' for the healing event, thus increasing the probability that a stable chromosome will be recovered. Correlative evidence from healed chromosomes in both yeast and humans indicate that normal occurrences of such sequences at internal chromosomal loci are the major sites of *de novo* telomere addition (Kramer & Haber, 1993; Harrington & Greider, 1991). (3) The *LYS2* gene is located on the telomere-proximal side of the *HO* site, and *HIS3* is located on the centromere-proximal side of the TG_{1-3} sequence. The combination of these two genes provides a strong genetic selection for the healing event. The loss of *LYS2*, and hence loss of the region distal to the cut site, is selected by growth on α -aminoadipate (α -AA) (Zaret & Sherman, 1985). Simultaneous selection for *HIS3* (growth in the absence of histidine) ensures that sequences centromere-proximal to the cleavage site are still present (Aparicio & Gottschling, 1994).

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The strain contains one additional difference, the *TLC1* gene is a conditional allele, under control of the *MET3* promoter. Loss of *TLC1* function is accomplished by turning off the *MET3* promoter (by the addition of methionine to the media), thus allowing the requirement for *TLC1* function in telomere healing to be tested.

It is expected that when *HO* endonuclease is expressed (by the presence of galactose in the medium) in *TLC1*⁺ cells, the VII-L chromosome will be cleaved at the *HO* site. Those cells that have formed a new telomere at or near the TG₁₋₃ 'seed' sequences, and have lost the distal *LYS2* gene (presumably to nuclease degradation, inability to replicate, or missegregation) will be selected on -his + α -AA plates. The selection will be imposed on the cells several generations after *HO* cleavage. This is to avoid phenotypic lag during α -AA selection, due to the initial presence of the *LYS2* gene product.

20

It is expected that *HO* endonuclease cleavage will occur in nearly 100% of the cells in the population (FIG. 8), and that at least 1/1000 cells will heal at the TG₁₋₃ 'seed' (Kramer & Haber, 1993). Those chromosomes that do not heal at the 'seed' may form a new telomere at a more centromere-proximal chromosomal position, or be completely lost. In the event an essential gene or the entire chromosome is lost, the cell is inviable; if a new telomere is formed at a viable chromosomal location, the cell will be His⁻. To verify that the telomere has indeed healed as expected, Southern analysis of the chromosome in this region is performed. When the study is repeated in the absence of functional *TLC1* gene product, it is expected that no growth will be observed on -his + α -AA media. In fact, the process of *HO* cleavage in *tlc1*⁻ cells may result in complete inviability, as the lack of telomerase activity to 'heal' the broken

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chromosome end may result in chromosome loss. If growth on -his + α -AA media is observed in *tlc1* cells, it may be the result of a loss of function mutation in the *LYS2* gene in a small subset of cells where cleavage did not occur (this is determined by Southern analysis).

Of course, the original diploid system developed by Haber may be used in this analysis. The assays used to characterize loss of *TLC1* and *EST1* function *in vivo*, namely a decrease in telomere length and cell viability with increased age of a culture (in a *rad52* strain), can also be used for further analysis (Lundblad & Blackburn, 1989).

EXAMPLE XIII

Genetic Dissection of *TLC1* RNA

The telomerase RNA molecule is dissected to identify regions that are essential for telomerase activity and to define regions that interact with other telomerase components. Two different genetic approaches are used. First, the technique that resulted in the original identification of *TLC1*, namely, overexpression of *TLC1* cDNAs to suppress telomeric silencing. Limited sequences within the RNA that are responsible for the suppression are defined. These regions will interact with other telomerase components and are useful in identifying these components.

Second, methods used to dissect small nuclear RNAs (snRNAs) and their function in yeast (Parker, 1989; Guthrie & Patterson, 1988) are adapted. Here mutants of *TLC1* are constructed and tested for *in vivo* functions, such as the ability to 'heal' broken chromosomes or form single-stranded tails late in S phase. Again, important regions of the RNA are identified and used to isolate interacting components.

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Methods to identify important regions of snRNAs include phylogenetic comparisons of each type of RNA (e.g. U1, U2, etc.) (Miraglia et al., 1991; Ares, Jr., 1986; Ares, Jr., & Igel, 1990). Conserved sequences and secondary structures in the RNA molecules of different species have been analyzed. Comparisons between telomerase RNAs from a variety of ciliates have suggested conserved secondary structures, while little conservation at the primary sequence level is detected (Lingner et al., 1995; Romero & Blackburn, 1991). So far, conserved sequences or structures between the 1.3 kb *TLC1* RNA and the much smaller ciliate RNAs (the largest is 200 nucleotides) have not been identified, but continued analyses may yield useful information. While a similar size difference is seen between the long U2 snRNA from *S. cerevisiae* and the smaller U2's in vertebrates, conserved primary sequences between U2 RNAs facilitated structural alignments that identified critical stems and loops in the RNA.

20

A. Minimal Sequence Elements in *TLC1* RNA that Suppress Telomeric Silencing

The same strains and expression vector used to identify *TLC1* cDNAs are used to identify limited regions of the telomerase RNA that suppress telomeric silencing. The full length telomerase RNA is examined to determine whether it has the ability to suppress silencing at high levels. While this molecule is expected to suppress very well, it is possible that only truncated, non-functional telomerase RNAs have this phenotype when overexpressed (a dominant-negative phenotype) (Herskowitz, 1987). Nonetheless, the full length RNA serves as the starting point for creating 5' and 3' deletion derivatives, as well as derivatives that either delete internal segments or retain a single internal element. It is contemplated that relatively small regions of the RNA (perhaps 50 bp)

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that suppress silencing will be identified. By reducing the size, an assured interaction of a single component and the RNA fragment is determined. This increases the likelihood of identifying the component.

5

It is believed that overexpression of *TLC1* causes suppression of telomeric silencing because the RNA titrates away a limited component in the cell. To determine whether the limited component is part of telomerase, part of the telomeric silencing machinery, or plays a role in both complexes, each of the *TLC1* overexpression derivatives are tested in other assays, e.g., in particular, the telomere 'healing' assay that can be performed quantitatively. The derivatives that have the strongest effect in reducing the frequency of healing are the best candidates for a telomerase-specific interaction.

This titration assay is contemplated for use in identifying telomerase RNA structures that are conserved between species. For instance, the telomerase RNA from a ciliate such as *Oxytricha* may act to suppress telomeric silencing when expressed at high levels, if the *Oxytricha* RNA is able to interact with a conserved telomerase component in yeast. If such structural conservation occurs, this assay is then useful for isolating telomerase RNAs from species in which the RNA has not yet been isolated, such as from humans.

30 B. Creating *TLC1* Mutants

A second method to identify important regions of the *TLC1* RNA that may interact with other telomerase components involves making loss of function mutations in the RNA, excluding the template region. With an RNA as large as the *TLC1* transcript, such mutations are relatively easy to isolate and, indeed, specific regions

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of the RNA will be mutated. Either site-directed or limited random mutations to regions of *TLC1* for which there is evidence of a conserved secondary structure, or for interaction with other telomerase components, are thus made. Such regions of *TLC1* RNA include those that can suppress telomeric silencing when overexpressed, or contain predicted secondary structures that are conserved between *TLC1* RNA and telomerase RNAs from other species. These mutations may define dominant, semi-dominant, or recessive alleles of *TLC1*.

Screening for recessive mutations is first advised because they can be more easily manipulated. Conditional alleles that are sensitive to temperature or moderate structural perturbations, such as low concentrations of formamide or D₂O, typically are of greater utility identifying interacting proteins than mutations which are complete loss of function (Huffaker et al., 1987; Bartel & Varshavsky, 1988). These alleles are isolated by a "plasmid shuffle" scheme (Sikorski & Boeke, 1991): One centromere plasmid that contains both the *URA3* and wild type *TLC1* genes is introduced into a strain deleted for the normal chromosomal copy of *TLC1* and containing the required genotype for the telomere 'healing' assay. A second centromere plasmid, with a different selectable marker such as *TRP1*, carries a mutated *TLC1* gene. The mutagenized plasmid(s) are then transformed in the appropriate yeast strain, and a screen for conditional alleles of *TLC1* is carried out.

Mutants of interest are those that allow a transformant to "heal" telomeres on -trp +FOA medium (losing the wild type *TLC1-URA3* plasmid and retaining the mutant version, which still functions) only when grown at the permissive temperature. At the nonpermissive temperature, such strains are unable to heal telomeres in the presence of FOA because healing is dependent on

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wild-type *TLC1* RNA (growth on FOA can only occur in the absence of the *URA3* gene product (Boeke et al., 1987)). The relative ability of these alleles to function in the healing assay is quantified by determining the frequency of chromosome healing. The quantitative analysis is useful in classifying the alleles and isolating either suppressors or enhancers. The *TLC1* alleles are also screened in other assays, such as formation of single-strand tails, to determine if there are mechanistic differences between the alleles.

EXAMPLE XIV

Isolation of Genes that Interact with *TLC1*

Based on the two types of *TLC1* derivatives created, genetic screens are carried out to isolate genes whose products interact with the telomerase RNA.

A. Genes that Re-Establish Telomeric Silencing when *TLC1* RNAs are Overexpressed

This approach is based on the model that when parts of the *TLC1* RNA are overexpressed, they interact with a limiting telomerase component to form a non-functional complex. This reduces the level of telomerase activity in the cell, causing reduced telomere length, and the reduction in telomere length decreases the frequency with which telomeric silencing complexes are assembled. Thus, if the concentration of the component is increased such that it is no longer limiting, telomeres become longer and telomeric silencing is re-established.

In this approach, the small *TLC1* fragment(s) are expressed at a level that is only slightly higher than necessary for suppression of telomeric silencing. This way, only a small amount of the limiting component is needed to re-establish silencing. The threshold

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concentration for the *GAL1-TLC1* RNA fragment to suppress telomeric silencing is determined by decreasing the concentration of galactose in the medium; expression from this promoter is modulated by galactose concentration.

5 The actual threshold is determined by measuring steady-state RNA levels as a function of telomeric silencing. If a threshold concentration is achieved, the construct is integrated into the genome to help keep the *TLC1* RNA fragment level constant.

10

Once a suitable concentration of the *TLC1* fragment is established, the gene encoding the limiting telomerase component is isolated by identifying an overexpression plasmid that, when introduced into this strain,
15 re-establishes silencing. Yeast plasmid libraries that may be used include high copy genomic libraries and cDNA libraries, e.g., driven by the *ADH1* promoter (obtainable from S. Elledge).

20 Candidate plasmids are isolated by a reversal of the selection procedure used to originally identify *TLC1*. The starting strain contains the construct that expresses the *TLC1* fragment at high levels in addition to having two telomeres marked, one with *ADE2* the other with *URA3*.
25 In this strain, telomeric silencing is suppressed by the expression of the *TLC1* fragment; the cells are sensitive to growth on FOA (*URA3*⁺), and are white (*ADE2*⁺). When silencing is re-established, the cells are able to grow on FOA (*FOA*^R; *ura3*) and form red/white sector colonies
30 (red=*ade2*). After the library plasmids are transformed into the strain, re-establishment of silencing is selected/screened by growth of red/white colonies on FOA. In addition to components that interact with *TLC1*, some plasmids may be isolated that affect the expression level
35 of the *GAL1*-driven *TLC1* fragment. This class is identified by examining the steady state level of the *TLC1* RNA fragment. This class may represent genes that

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negatively regulate *GAL1* transcription, or genes that regulate RNA stability.

However, it is also possible that more than one gene product may be limiting in the titration; for example the RNA fragment may be bound by a dimeric complex, with the two components at low concentration in the cell. The limiting factor may be lethal to yeast cells at high concentration, "fouling" an essential cellular function. Therefore, the *TLC1* RNA fragment may be used to probe a *lgt11* yeast cDNA expression library. An *in vitro* synthesized ³²P-labeled RNA, identical to that defined *in vivo*, is used to probe a set of filters containing phage plaques. Those plaques that contain a cDNA expressing a *TLC1* interacting protein are isolated by virtue of their ability to bind the radioactive probe.

For those plasmids that are candidates for encoding a *TLC1* interacting component, the DNA necessary for the effect is determined and subjected to sequence analysis. Putative genes are then subjected to the same analyses used to identify *TLC1* as a telomerase component. That is, examining telomere length and cell viability in a strain with a null mutation of the gene and the gene is characterized in biochemical analyses.

B. Modifiers of Conditional *TLC1* Mutations

A more classical approach for identifying components that interact with telomerase RNA may be used, e.g., by isolating mutations that enhance or suppress the phenotypes of conditional alleles of *TLC1* (as created above). This genetic approach has been successfully utilized in identifying components from many complex biological systems, including proteins that interact with snRNAs involved in splicing (Parker, 1989; Guthrie & Patterson, 1988).

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Mutations that suppress the defect of telomere healing in conditional alleles of *tlc1* under non-permissive conditions are isolated. The starting strain includes the "healing" set-up in addition to a specific conditional allele of *tlc1*. At non-permissive temperatures, this strain is unable to grow on -his+ α -AA medium after *HO* endonuclease induction (or as noted, induction may be lethal), the result of a defect in telomere healing. This strain is then mutagenized and mutations that permit 'healing' to occur (growth on -his+ α -AA medium) are isolated. The strains containing the suppressors are back-crossed to a parent strain (congenic with the starting strain except the opposite mating type) and the resulting diploid is sporulated and tetrads dissected. After several such backcrosses to isolate the suppressor mutation from other mutations that may have been introduced during mutagenesis, the suppression phenotype is checked to see that it segregates 2:2. Once isolated, the suppressor is crossed to strains containing other *tlc1* alleles to determine if it acts specifically on the allele from which it was isolated. If there is allele specificity, then the suppressor mutation interacts with *TLC1* RNA *in vivo* (Huffaker et al., 1987). If not, there is still a high probability that the suppressor interacts with *TLC1*. Possible suppressor linkage to *tlc1* mutations are also determined.

The strategy to isolate the gene encoding the suppressor depends on whether the mutation is dominant, semi-dominant, or recessive, and whether the mutation has additional phenotypes that may be followed. Dominant mutations are currently preferred. A centromere-based genomic DNA library made from the strain containing the suppressor is used to transform the non-mutated 'healing', *tlc1* strain. Those plasmids that permit

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telomere healing, as described above, and do not encode the wild type *TLC1* gene, carry the suppressor gene.

5 An alternative method is to isolate genes that suppress a mutation when in high dosage (Bender & Pringle, 1991). Suppressors can thus be screened for by transforming with a high copy genomic library and isolating plasmids that suppress the telomere healing defect.

10

Enhancers of the conditional *TLC1* alleles grown at permissive or semi-permissive temperatures may also be isolated, as has been successful in identifying interacting components within many biological processes of yeast (Frank et al., 1994).

15

C. Continued Characterization of the *STR* Genes

20 Two of these genes, *STR5* and *STR6* have a much stronger affect on telomeric silencing than on silencing at *HML* though not as strikingly as *TLC1* does (Example X; FIG. 7A, FIG. 7B). If null mutations of these genes have similar effects on telomeres as those seen in *tlc1*⁻strains, they are excellent candidates for being components of telomerase.

25

EXAMPLE XV

BIOCHEMICAL APPROACHES TO TELOMERASE

30 Telomere DNA binding proteins from *Oxytricha* have been isolated and characterized (Gottschling & Zakian, 1986). *In vitro* transcription assays with yeast extracts and proteins have also yielded low abundance transcription factors (Parthun & Jaehning, 1992). Therefore, protein elements of telomerase are isolatable.

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**A. Biochemical Characterization of the
Ribonucleoprotein Complex Associated with *TLC1* RNA**

To examine the physical association of genes with
5 *TLC1*, procedures used to isolate small nuclear
ribonucleoprotein particles (snRNPs) are adapted
(Luhrmann, 1988). The approximate steady state
concentration of *TLC1* RNA within cells is first
10 determined, by comparing the amount of the RNA isolated
from a given number of cells with a dilution series of *in*
vitro transcribed *TLC1* RNA. The information obtained
from this analysis indicates how much telomerase activity
and associated protein is in a cell, and serves as an
15 indicator for enrichment of the *TLC1* ribonucleoprotein
complex during fractionation procedures.

The first fractionation step separates the nucleus
and the cytoplasm, using procedures described for other
ribonucleoprotein complexes in yeast (Hopper et al.,
20 1990). It is expected that all *TLC1* RNA will be
localized to the nucleus, however a cytoplasmic location
is not excluded. In the event *TLC1* RNA is in the
cytoplasm, the fractionation is performed on cells that
are arrested at various points in the cell cycle (with
25 pheromone, *CDC* mutations, or chemicals).

Next, with RNA in the nucleus, a nuclear extract is
made and fractionated to give a *TLC1* RNA associated
particle e.g., by a combination of gradient
30 centrifugation methods (equilibrium and sedimentation
velocity), column chromatography steps, including
gel-filtration, ion-exchange, hydrophobic/ion-exchange,
and agarose beads linked to dyes and other ligands, and
gel electrophoresis (Luhrmann, 1988). In addition,
35 buffer and ion conditions are carefully monitored as they
can affect the stability of the particle (Roth et al.,
1991). An affinity column for *TLC1* RNA is also

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contemplated, e.g., as is created by synthesizing a biotinylated DNA oligonucleotide that is complementary to the RNA's template sequence. The oligonucleotide, which will hybridize to the RNA in the particle, is then
5 tethered to streptavidin beads (Kijas et al., 1994).

As a first use of the fractionation, the fate of *EST1* may be followed using protein anti-*EST1* antibodies (available from Dr. V. Lundblad) as genetic evidence
10 suggests that it may be part of or regulate telomerase (Lundblad & Szostak, 1989). It is contemplated that extracts from two different mutants that both have 'defective' particles will be combined to generate a fully assembled particle, thus allowing insights into the
15 particle's biogenesis.

Reagents, such as antibodies, to proteins identified in the genetic screens are also contemplated.

20 **B. *In vitro* Assay for Telomerase Activity from *S. cerevisiae***

Telomerase activity has been biochemically identified from several ciliates and vertebrates,
25 including human cells. However, prior to the present invention, telomerase activity had not been biochemically detected in *S. cerevisiae*. Now assays are available, based partly on those previously described (Greider & Blackburn, 1985; Mantell & Greider, 1994; Prowse et al.,
30 1993; Autexier & Greider, 1994; Greider & Blackburn, 1987), in which a DNA oligonucleotide substrate, representing the 3' G-rich telomere tail, is incubated in extracts with ³²P-labeled dNTP's (typically dGTP or dTTP). The products of telomerase elongation on the
35 input oligonucleotide substrate are then detected by gel electrophoresis and autoradiography.

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Identifying the TLC1 RNA and its sequence will likely assist in isolating the activity. To identify telomerase activity in yeast, buffer conditions that have been successful in other systems are used and damaging
5 nucleases are removed. In addition, extracts from strains that are deficient in several of the major proteases (Jones, 1991), and use cocktails of protease inhibitors that have been successfully used for in vitro transcription (Parthun & Jaehning, 1992) are employed.

10

A series of substrates, ones that are perfectly complementary to the template, are truncated on their 3' end by one or a few nucleotides, or are simply alternating tracts of (GT)_n are used in isolation
15 studies, and very short oligonucleotide products are also analyzed. As telomerase activity in yeast may be very tightly regulated, and limited to only a brief period of the cell cycle, (Wellinger et al., 1993), extracts from cells isolated in a synchronous population late in S
20 phase are also to be used.

* * *

All of the compositions and methods disclosed and
25 claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations
30 may be applied to the composition, methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents that are both chemically and
35 physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and

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modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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SINGER, Miriam S.

(iii) TITLE OF INVENTION: Telomerase Compositions
and Methods

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(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

(D) SOFTWARE: PatentIn Release #1.0,

35

Version #1.30

(vii) CURRENT APPLICATION DATA:

- 236 -

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: CONCURRENTLY HEREWITH
- (C) CLASSIFICATION: UNKNOWN

5 (viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: SN 08/431,080
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- (C) CLASSIFICATION: Unknown

- 10 (A) APPLICATION NUMBER: SN 08/326,781
- (B) FILING DATE: 20-OCT-1994
- (C) CLASSIFICATION: Unknown

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25 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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20	TTCTCGTTTT CTTATACCTA GTATTTTTTC TGACACTGTT TAAGGTGACA GAAAAAAGG	600
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- 238 -

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GGCAAGGGTG TCCTTTCTTA AGCATCGGTT AGGTTTGCGG GCGATCAGTA ACTGAACAAT 960

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AATCGCGCGT ACTGTACTTG TATATCGCTT TATAAGCGCT TTTAATTGAT TGTTTCATGAC 1260

20 GAGGATAGGC GGATAGGCGG AGGTATGCCT CTTAATATTT A 1301

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10

GTGTGTGGGT GTG

13

(2) INFORMATION FOR SEQ ID NO:3:

15

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACCACACCC ACACAC

25

16

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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5 TAAATATTAA GAGGCATACC TCCGCCCTATC CGCCTATCCT CGTCATGAAC ATCAATTTAA 60
AAGCGCTTAT AAAGCGATAT ACAAATACAG TACGCGCGAT TTCTACAATA CAAAAAATAT 120
ACATCAAGAA AAAAAATGTT TCCAAAAATT ATCTAAATGC ATCGAAGGCA TTAGGAGAAG 180
TAGCTGTGAA TACAACACCA AGATTTCATAA AATGAACACA CGGTTCCCTC CGCTTGGAAG 240
ATAATGCGAC AAAAAATACCG TATTGATCAT CAAAGTAGTT TTAATAGATA CCTAAAAAAA 300
CCATCTTGAA AAATCTCAA TTACGTTCTT GATCTTGTGT CATTTGTCAG TTAATGATCG 360
CCCGCAACC TAACCGATGC TTAAGAAAGG ACACCCCTTG CTTTGGGCTT ATTTACCTAC 420
TCGTATTTTT CTCTGTCACA TCGTTCGATG TACGGGGCAC ATTTGGAAT TTCATCAGTA 480
AGTTCAGTGA ATAGATTTTT TATTTTACCT TTTTGTAGTG GGATTTATTC TTTTAAAGGC 540
AAAAATCTAC TGAATAAACG GAAAAAATA GAATAAACCA TTTCTATATA TACTCATGTT 600
CCCTGACGTT CTTTTTCCTT TTTCTTTTTT CAGAGTTAAC GATAAGATAG ACATAAAGTG 660
ACAGCGCTTA GCACCGTCTG TTTGCAATC TAACTTAAC TCCTTTTTTT CTGTCACCTT 720

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AAACAGTGTC AGANNAATA CTAGGTATAA GAAACGAGA AAAAAATANA CAGCGAACTC 780
GTGCAAACTT TGCTAATAAA CAATTAGCTG TAACATTTGT GTGTGGGTGT GGTGATGGTA 840
5 GGCTTCCCAT GGTAATTAAA AGGTTAGGTC GAGAAGAGGA TCGGTACGNA GAAGGAATAA 900
CAGGAATAAG TTCAAAAAACA CTGCTTTAGC AACTAAATGC AATAGCAGTG TTTAAGAATT 960
TACGGTTTGC ATTTTCTAAA CTCAGATTTT AGCCATCTAT AAGTAGAAAC ACAATAAAAA 1020
10 ACCACAAATT GGCACACAC AAGCATCTAC ACTGACACCA GCATACTCGA AATTCTTTGG 1080
AAAAGAAAAG AGCAGCAGGC TATCAACTGA AAGATCAATC CGAAATCCGA CACTATCTCT 1140
TCACCATCGA GTGCCTACCA AATTCTGAG GCCTGCATGA TGGAAAACTC AAACGTAGAA 1200
TGTAACAAAA ACACGGACTG AAAAAAAAAA AAATACGATT AAGCAAAACGC AACAGCCATT 1260
GACATTTTCA TAGGGTACCT ATCTTCCTCT CTAGTTTAT T 1301

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

TAATTACCAT GGGAAGCCTA CCATCACCAG GCCCACACAC AAATG 45

(2) INFORMATION FOR SEQ ID NO:6:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 CCGGAATTCA TACGAAGATG ATGATTAAAT C 31

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GGCTTGCCAT AGACTTGCTC G

21

(2) INFORMATION FOR SEQ ID NO:8:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGTAATC TCCGAA

15

16

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGACGACTG TCGTCCGTCA AAAAAATTC AAGGAAACCG

40

30 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 244 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGACGACAG TCGTCCGCAG AAGGAAGAAC GAAGGAA

37

5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

15

CGAACGGATC CCCTTCAGCC ACTACAGCCT ACTT

34

(2) INFORMATION FOR SEQ ID NO:12:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAAGGGATC CGCCAATTGC GAATGCACTC ACCG

34

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5

CCGGATCCTG CCTCGGTAAT GATTTCATT TTT

33

(2) INFORMATION FOR SEQ ID NO:14:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGGATCCTC TCGAGTTCAA GAGAAAAAAA AAGAAA

36

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 1882 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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60
GATTTTATA AGTTA/ACTT GTGTACATGT TATTCTACT TAGTTATTCA TACTCATCGT
120
TAAAAGCCGT TCNAAAGTCCC TCATCTGGTA TACTTACCCG GGTACCTCT GTTCTTCCTA
180
CCTCTTGCAG CAGGGCTGNA TAAACTTTTCG TCCACATCCT CCATCACTGT TGATATATAA
240
TACTCTCCGC CACTATGCGT CCATGAAACA CTATCCTCCT TAAGATCATA CCTTTGCACC
300
TTTAATCTAT TGAAGATGTT CTCAACATTG TAGAAGTTGA TCTGATAAGT GAGGCTTCTT
360
AAACTTTTCA AACTTATGAT CTTACATCCA ACTTTTGCCG TTTGTAGTAT CTTTTCGACT
420
TTTTTTATTCA AATCTTCATC AAATAAAAAA TTATTACGA GGATAACATC GCACTGAGGA
480
ATTAGTTCAG CGACCCCTGTT ATTGTCCACA AAGCTTTTCT TCAATGAAAA CTCCACGTTG
540
TTCNAAACGA TCCCATATAA CTTACACCTC TTCTTTAGTT CCTCGTACTG CAGTATAGTT
600
AAATCGCTAG CATCATCCAT GATTTACAT CCGAAGCTTA ATGCACATCC ACATTCCAAC
660
GCAGCTTGTA CTACGCAATT ACCTACTCCC GNACCGAGAT CCATGAAAGT GTCACCCCTC
720
TTCAACTGGC ATTGTTGATA TACATCAGAT AGGAAATTGG GCNAAAGTTC TCCATAAACA

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TAATTGCTGA ATGCTTTTCTTA ATGTTTCAAT TTATTGCGCT GCGGATGGAT ACTCCTGGTA 780

TAGACGATAT GCAAGAGATC ATGAATGAAT GAACGAGGAA TTTTATCAAT TGTTCCTAAA 840

5 TGGTCAATTA TTCCTTGCCT AGGAATTTC A GAATCATT TGTTCATATA ATTTATAGCA 900

TTCACGAAAC CTTTCGTGTC AGAGTTATCA AATGATGCAT TTAGGTCGG TAGTATAGTT 960

TCCTTCAATT GTTCAGCATA AGTGAAGGT AAAAGAGCCA GGCAGCTGTA TTCAATTAAAT 1020

10 TTACCAATTT CACTCATTTG ATTATAAATG GCTGTTGACC TTTTGAAGTC GACTTTGTAC 1080

TCTTCCATAT AATTGAAAA TAAATACTC TGCAACTTTG CTGTCGTTAC TGAGGAAGTG 1140

15 TCGTTATCTG ATGTCAAGCT CGTTGGCTGT GGAGAAATTTG TTCTTAAACT AATGGATTGT 1200

ATAGGAGTTC CAGATATAT TTCATGTGAT CTAAAGTACT CTATGTCAAA TAATGGATAT 1260

TGTAACCGTA GACACGGGCC ATTCCAATCA ACAAATGTTG ATGAAGGACT ATCGCGATCA 1320

20 TTCTTCTTGT TTGCCCGACC TTTTTCATAT GGCTTTTTTT CTGCTGCAGT ATCTATTCT 1380

TGCTTTGAAA TTGGGGTATG TTTATGGTTA GTCCTGCCAT TTTTTCCTTT TACTTTTGCA 1440

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10
5
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GCTTTTGGCT TCTTTTACATC CTTCCTTCGTG GTGGTAGATG ACTTCTTCCT TGTTGTTTCTA 1500
TTATTGGTTT TCTTGTGAAT GGGAGGTATA ACCTTCTCCA CCAGCGGAAC CAAACCCATTA 1550
TCCTTACCCT TGGTGTTTCT ATCTCTTAAA AATCCTCGAG GTAAAGATGA CCCATATATT 1620
GGATCGTATT TATTAGCTTC TTCTAATAAA TTTTGTAATT GCTTAGAGAG AAGCGTACCT 1680
TTAGAATAGC TTGAAAGCGA CTGGGTTTGC ATATCGGTGC CTTTCTTCTC ATCAATAGGT 1740
GATATTGAAG ATTCCTGAGA GTCTAAGTTG GGGGACGACA TAATGAATGA GTCTGAGTTA 1800
TTATTTGATA TACTTTCTTG ATCGCCCATT ACTGTACAAC AAAATGTAAC CAAAGCGCAC 1860
AATTACTGGT GACCTCCTTG AT 1882

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	Met Gly Asp Gln Glu Ser Ile Ser Asn Asn Asn Ser Asp Ser Phe Ile	15
1	5	10
10	Met Ser Ser Pro Asn Leu Asp Ser Gln Glu Ser Ser Ile Ser Pro Ile	30
	20	25
	Asp Glu Lys Lys Gly Thr Asp Met Gln Thr Lys Ser Leu Ser Ser Tyr	45
	35	40
15	Ser Lys Gly Thr Leu Leu Ser Lys Gln Val Gln Asn Leu Leu Glu Glu	60
	50	55
	Ala Asn Lys Tyr Asp Pro Ile Tyr Gly Ser Ser Leu Pro Arg Gly Phe	80
	65	70
	Leu Arg Asp Arg Asn Thr Lys Gly Lys Asp Asn Gly Leu Val Pro Leu	95
20	85	90

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Val Glu Lys Val Ile Pro Pro Ile His Lys Lys Thr Asn Asn Arg Asn
 100 105 110

Thr Arg Lys Lys Ser Ser Thr Thr Thr Lys Lys Asp Val Lys Lys Pro
 115 120 125

5

Lys Ala Ala Lys Val Lys Gly Lys Asn Gly Arg Thr Asn His Lys His
 130 135 140

Thr Pro Ile Ser Lys Gln Glu Ile Asp Thr Ala Arg Glu Lys Lys Pro
 145 150 155 160

10

Leu Lys Lys Gly Arg Ala Asn Lys Lys Asn Asp Arg Asp Ser Pro Ser
 165 170 175

15

Ser Thr Phe Val Asp Trp Asn Gly Pro Cys Leu Arg Leu Gln Tyr Pro
 180 185 190

Leu phe Asp Ile Glu Tyr Leu Arg Ser His Glu Ile Tyr Ser Gly Thr
 195 200 205

20

Pro Ile Gln Ser Ile Ser Leu Arg Thr Asn Ser Pro Gln Pro Thr Ser
 210 215 220

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Leu Thr Ser Asp Asn Asp Thr Ser Ser Val Thr Thr Ala Lys Leu Gln
 225 230 235 240

Ser Ile Leu Phe Ser Asn Tyr Met Glu Glu Tyr Lys Val Asp Phe Lys
 245 250 255

5

Arg Ser Thr Ala Ile Tyr Asn Pro Met Ser Glu Ile Gly Lys Leu Ile
 260 265 270

Glu Tyr Ser Cys Leu Val Phe Leu Pro Ser Pro Tyr Ala Glu Gln Leu
 275 280 285

10

Lys Glu Thr Ile Leu Pro Asp Leu Asn Ala Ser Phe Asp Asn Ser Asp
 290 295 300

15

Thr Lys Gly Phe Val Asn Ala Ile Asn Leu Tyr Asn Lys Met Ile Arg
 305 310 315 320

Glu Ile Pro Arg Gln Arg Ile Ile Asp His Leu Glu Thr Ile Asp Lys
 325 330 335

20

Ile Pro Arg Ser Phe Ile His Asp Phe Leu His Ile Val Tyr Thr Arg
 340 345 350

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Ser Ile His Pro Gln Ala Asn Lys Leu Lys His Tyr Lys Ala Phe Ser
 355 360 365
 Asn Tyr Val Tyr Gly Glu Leu Leu Pro Asn Phe Leu Ser Asp Val Tyr
 370 375 380
 Gln Gln Cys Gln Leu Lys Lys Gly Asp Thr Phe Met Asp Leu Gly Ser
 385 390 395 400
 Gly Val Gly Asn Cys Val Val Gln Ala Ala Leu Glu Cys Gly Cys Ala
 405 410 415
 Leu Ser Phe Gly Cys Glu Ile Met Asp Asp Ala Ser Asp Leu Thr Ile
 420 425 430
 Leu Gln Tyr Glu Glu Leu Lys Lys Arg Cys Lys Leu Tyr Gly Met Arg
 435 440 445
 Leu Asn Asn Val Glu Phe Ser Leu Lys Lys Ser Phe Val Asp Asn Asn
 450 455 460
 Arg Val Ala Glu Leu Ile Pro Gln Cys Asp Val Ile Leu Val Asn Asn
 465 470 475 480

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Phe Leu Phe Asp Glu Asp Leu Asn Lys Lys Val Glu Lys Ile Leu Gln
 485 490 495
 Thr Ala Lys Val Gly Cys Lys Ile Ile Ser Leu Lys Ser Leu Arg Ser
 500 505 510
 Leu Thr Tyr Gln Ile Asn Phe Tyr Asn Val Glu Asn Ile Phe Asn Arg
 515 520 525
 Leu Lys Val Gln Arg Tyr Asp Leu Lys Glu Asp Ser Val Ser Trp Thr
 530 535 540
 His Ser Gly Gly Glu Tyr Tyr Ile Ser Thr Val Met Glu Asp Val Asp
 545 550 555 560
 Glu Ser Leu Phe Ser Pro Ala Ala Arg Gly Arg Asn Arg Gly Thr
 565 570 575
 Pro Val Lys Tyr Thr Arg
 580

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10	GTCTTCTTCA TTCTCATAAA ATGCATTGCC TGTTTTGGCT TGATTGTCTA CATTTCATG	60
	ATCTTCAATT TCTCCTCTCG ATTTTGTGTT ATCATTCTTC CCACAACTTT CCTGGGCTCC	120
	ACTTTTTTGA TTGGTGTTGC CTTGAATTGT TATCTGACTC TCACCTCTGC GTTCTCTCAAC	180
15	ATACTTTTGA GTTAAAAATAT CTATCAAAGA GTCATCGCCA TCGTTGCTAT CTCCTGTGTA	240
	ATCCATTTTA TCTACTTCTT CTGCATTAC CTCTGCTTTT TTTTCAACGT TGGGTGCCTT	300
20	GATGGGTGAA GATGGCAAAT CGCTGAATTT CGTTATCGTC GGTTTATAG TTAAATCGCC	360
	CTCTATATCA TCGAGNATAT CATCTATATT ACGGAGAGAC TCCCTGGTAG ATATTCTGC	420
	TGGTTTAGGA CGCAGTTGCT CATTTCATT TTCTTGAATG AGTTGATTGA CGTCAGCGTT	480

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GGGTACTTGG ATATTTGTGA AACTAAGAAC AGTTTTCAGT CGATTAGGGA CTATAGGTGT 540
AGAAGAGGGA TTTTGGACAT CTTCTGTAGTC ATCAGAGTAT TCGGCAGCGC TTGTTGTTTT 500
5 GTCGGACATA TCTCGTTGTA AAGGTGAATA TTTCCATATT ACTTCTTCCA TGGGGCCGTC 660
CTCGTCTTGA GTGAAATCGT GATGCCCTACT CAAATTAGAC ATTCCCCGTT TCGGTTTAAAC 720
TTGTGAATTT GGTAATTGCT TTACGCTCTT GCTAACTGCT TTGTTTATAT CTTTGTGTTCT 780
10 TGATGTATTT CGTACTTGTG AAACGGCTAT TGACTTTAGG ACACTTGCAT TGGATACCTT 840
GGTGTCTTTC CCATTTAAGT TATTTATAGG AGCAAAAGCA TACTTTTTTT TCCTCTTAGT 900
15 TTGCTTAGAT AATATCGCCT TTGAATCATT TTGTATTATT TCTTTTTCCT CTGTCCTTCTT 960
CGCAGGTGAA ACAGATATAC TCGCAGACCT CTTGTTCCTC TGTGGCGTTC CGGGCAFCCT 1020
GACGATCTCT TCAATTGTCA GTGTTTGCTT GCACAAAATG AGTACTCACT TGAGTATGTT 1080
20 TTCTCCCAAT TTTC 1094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10

Met	Pro	Gly	Thr	Pro	Gln	Lys	Asn	Lys	Arg	Ser	Ala	Ser	Ile	Ser	Val
1				5				10					15		

Ser Pro Ala Lys Lys Thr Glu Glu Lys Glu Ile Ile Gln Asn Asp Ser

20 25 30

15

Lys Ala Ile Leu Ser Lys Lys Gln Thr Lys Arg Lys Lys Tyr Ala Phe
35 40 45

Ala Pro Ile Asn Asn Leu Asn Gly Lys Asn Thr Lys Val Ser Asn Ala

50 55 60

20

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Ser Val Leu Lys Ser Ile Ala Val Ser Gln Val Arg Asn Thr Ser Arg
65 70 75 80

Thr Lys Asp Ile Asn Lys Ala Val Ser Lys Ser Val Lys Gln Leu Pro
85 90 95

Asn Ser Gln Val Lys Pro Lys Arg Glu Met Ser Asn Leu Ser Arg His
100 105 110

His Asp Phe Thr Gln Asp Glu Asp Gly Pro Met Glu Glu Val Ile Trp
115 120 125

Lys Tyr Ser Pro Leu Gln Arg Asp Met Ser Asp Lys Thr Thr Ser Ala
130 135 140

Ala Glu Tyr Ser Asp Asp Tyr Glu Asp Val Gln Asn Pro Ser Ser Thr
145 150 155 160

Pro Ile Val Pro Asn Arg Leu Lys Thr Val Leu Ser Phe Thr Asn Ile
165 170 175

Gln Val Pro Asn Ala Asp Val Asn Gln Leu Ile Gln Glu Asn Gly Asn
180 185 190

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Glu Asn Val Asp Asn Gln Ala Lys Thr Gly Asn Ala Phe Tyr Glu Asn
325 330 335

Glu Glu Asp

5

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2434 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAAATCCC CTGCAGTTCA ATGCTGCAAT GATCTCTAAC AAATCGAATA ATAATGATAC 60

20 TTCCGCCGCG CCGGAAAATA GCTCGTATAT TGTGATAGGA AAACAGCATA ATAACAATAG 120

TAATAGCACA GCTATTGCTG CAACGGCCGA ATCCAAGCAA ATAAAAAGAAA ATAAC TTGAT 180

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AGACAGGCCA AACGGAAAGA AACCCMACAC TGTTCCTAAA TCTATGGCTG AAGCTTTATT 240
GTTGTATACT TCTAANAATG A'ANAAGATGC TGCAGATGCT ACTGTGTCCTA AGAAGTCAGC 300
5 GGAGCTTTCT ACGGAGCTTT CTACGGAGCC TCCTTCCTCT TCTTCGGAAG ATGTCAAAGT 360
AGGAAAAGAG GAAGAGGAAG AGGGTGAAT ATTTTCATGAG GCAAGAGACT ATGTAGAACC 420
CCGAAAAGCT AGTTTGAAGG AACGCGACAA CGCAGATAAG GCGGATGGTG AAGACATCGG 480
10 CGAAGACATC GGTGAAGACA TCGGTGAAGA CATCGGTGAA GACATTGGTG AAGACATTGG 540
TGAAAACCTG GGTCTCTCCAT TAGCAACCAT TGATGATTCA TCTAATGAGA ATGAAAAGGA 600
15 AAAAAAGAAAG GAACTGTCTA CAAGCATTAG CAGTGATGAC GAAATAGAAG ACGACGAGGA 660
TGAGGATGAC ATGGATTATG ATTCTAGTGC TATGGAAAAA GAGCTCCCTG AAGAAGAGGA 720
GAGCGATTCC AGCTCCAAAA TTTCTGAAGG CGAAAAAAG AGTTTATATC AAGATTTAAT 780
20 GGAAAATAGT ACAGTGGAG TAAATCGGTA CGAACCAGTA AACAAACACCA AAGAAAATGG 840
AAACAGGAAT CCAAAGGGAG AGGAGGAGGA AGAAGAGGAA GAAGAGCTGA AACATANAATC 900

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960 TAGGTCAATC ACCCTCCGG TTACAATATC AAATCTATCA AACTTTTACC AATTCAATGA
1020 AAATATCAAT GATCGTGGTT CTTTAAACTC TACTAGAATT GTTAAAAATT GGGCGGACAA
1080 ATTACCAAT TTGAAGCCTC GTGGCCTTTT GAATCAIGGT GTTACTTGTT ACACAAATGC
1140 TGCTGTACAG GCTATGTTAC ACATTCCTTC GATACAACAT TATCTTTTGG ATATACTAAT
1200 GGGGAAATAC GATAGCACCA TCTCAAAAAA TTCCGTTTCC TATACTTTAG CTGAAACAAG
1260 TAAAAAATG TGGTTACCG TCTCAAAAAA CCCTAGAAAG AACGTTTCAG CTTCTTACAT
1320 TAATCCAAA CATTGTGATT CCAGATTGGA TGACATTAAT TGTATGATGA GCGAATGSCA
1380 GCAGGAAGAT TCACATGAGT ACTTCATGTC TCTGATGICA AGATTACAGG AAGATTCTGT
1440 TCCCAAGGT CATAAACTTA TAGAATCGAT AATATATGAC ATATTGGTG GTCTTTTAAA
1500 GCAGATCGTT ACTTGCAAAT CTTGTGGCAG TATATCTAAA ACAGAACAAC CATTTTACGA
1560 TTTATCGTTG CACTTGAAAG GGAAGAAAAA ACTTGATCCA AATTCTGACC TGTCGAGTGA
1620 TAGCATTAAAC GGCACCTTCAG CCACCACCTC TACCACCTACC TCCAATGCTG CCACAAAACC

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ATCTCTTTCA TCCTCTTCAT CTGTCAATTT AAACAATGGC TCACCATTGG CCGCTGCCAG 1680
TGATTTAAGT TCAGCCCAACC GCAGATTTTC TATTGAAAAA TCAATTAAAG ATTCTCTTCAA 1740
5 TCCCCGAATTA ATCAAGGTTG ACAAGGAGCA AAAGGGTTAC GTTTGTGAGA AGTGTCACAA 1800
GACCACGAAC GCCGTGAAGC ATAGTTCAAT ATTAAGGGCT CCTGAAACTT TACTTGTGCA 1860
TCTGAAAAAA TTCAGATTCA ATGGCACGTC CTCATCAAAA ATGAAGCAAG CTGTTTCTTA 1920
TCCTATGTTT TTAGATTTGA CGGAATATTG TGAGAGTAAA GAGCTACCTG TCAAAATACCA 1980
ACTATTAAGC GTGGTGGTTC ATGAGGGCCG CTCCTTTTCT TCAGGTCACT ACATTGCCCA 2040
15 CTGCAAGCAA CCAGACGGTA GCTGGGCCAC TTACGACGAC GAGTATATTA ATATAATATC 2100
TGAAAGGGAC GTTTTAAAGG AACCCCAACGC ATATTATCTC CTATACACGA GGCTAACTCC 2160
AAAATCGGTT CCATTGCCAT TGGCGAAATC TGCCATGGCC ACTGGTAATG TTACCTCTAA 2220
20 ATCCAAACAG GAACAGGCTG TTAACGAACC AAATAACCGC CCATTGAAGA TTAATAGCAA 2280
GAAAAATAAC AGAAAAAAAT GGAAAAAAAT AAAAAAGGA AGTTCACCAA ATGAAAAAAC 2340

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TCGATATTCC TGGATTTC TCTTTTCATA GGCAATTTTA TTAGCAATTC ATTTTATTA 2400
TACCAAATCA ATATATACAT ATAAAGGCCT TCGT 2434

5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15

Ser Asn Pro Leu Gln Phe Asn Ala Ala Met Ile Ser Asn Lys Ser Asn
1 5 10 15

Asn Asn Asp Thr Ser Ala Ala Pro Glu Asn Ser Ser Tyr Ile Val Ile
20 25 30

Gly Lys Gln His Asn Asn Ser Asn Ser Thr Ala Ile Ala Ala Thr
35 40 45

20

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5 Ala Glu Ser Lys Gln Ile Lys Glu Asn Asn Leu Ile Asp Arg Pro Asn
 50 55 60
 Gly Lys Lys Thr Asn Thr Val Pro Lys Ser Met Ala Glu Ala Leu Leu
 65 70 75 80
 Leu Tyr Thr Ser Lys Asn Asp Lys Asp Ala Ala Asp Ala Thr Gly Ala
 85 90 95
 10 Lys Lys Ser Ala Glu Leu Ser Thr Glu Leu Ser Thr Glu Pro Pro Ser
 100 105 110
 Ser Ser Ser Glu Asp Val Lys Val Gly Lys Glu Glu Glu Glu Gly
 115 120 125
 15 Glu Ile Phe His Glu Ala Arg Asp Tyr Val Glu Pro Arg Lys Ala Ser
 130 135 140
 Leu Lys Glu Arg Asp Asn Ala Asp Lys Lys Gly Asp Gly Glu Asp Ile Gly
 145 150 155 160
 Glu Asp Ile Gly Glu Asp Ile Gly Glu Asp Ile Gly Glu Asp Ile Gly
 165 170 175

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Glu Asp Ile Gly Glu Asn Leu Gly Ser Pro Leu Ala Thr Ile Asp Asp
 180 185 190

Ser Ser Asn Glu Asn Glu Lys Glu Lys Arg Lys Glu Leu Ser Thr Ser
 195 200 205

Ile Ser Ser Asp Asp Glu Ile Glu Asp Asp Glu Asp Glu Asp Met
 210 215 220

10 Asp Tyr Asp Ser Ser Ala Met Glu Lys Glu Leu Pro Glu Glu Glu
 225 230 235 240

Ser Asp Ser Ser Ser Lys Ile Ser Glu Gly Glu Lys Lys Ser Leu Tyr
 245 250 255

15 Gln Asp Leu Met Glu Asn Ser Thr Val Glu Val Asn Arg Tyr Glu Pro
 260 265 270

20 Val Asn Asn Thr Lys Glu Asn Gly Asn Arg Asn Pro Lys Gly Glu Glu
 275 280 285

Glu Glu Glu Glu Glu Glu Leu Lys His Lys Ser Arg Ser Ile Thr
 290 295 300

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5
 Pro Pro Val Thr Ile Ser Asn Leu Ser Asn Phe Tyr Gln Phe Asn Glu
 305 310 315 320
 Asn Ile Asn Asp Arg Gly Ser Leu Asn Ser Thr Arg Ile Val Lys Asn
 325 330 335
 Trp Gly Asp Lys Phe Thr Asn Leu Lys Pro Arg Gly Leu Leu Asn His
 340 345 350
 Gly Val Thr Cys Tyr Thr Asn Ala Ala Val Gln Ala Met Leu His Ile
 355 360 365
 Pro Ser Ile Gln His Tyr Leu Phe Asp Ile Leu Met Gly Lys Tyr Asp
 370 375 380
 Ser Thr Ile Ser Lys Asn Ser Val Ser Tyr Thr Leu Ala Glu Thr Ser
 385 390 395 400
 Lys Lys Met Trp Leu Pro Val Ser Lys Asn Pro Arg Lys Asn Val Ser
 405 410 415
 Ala Ser Tyr Ile Asn Pro Lys His Leu Ile Ser Arg Leu Asp Asp Ile
 420 425 430

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Asn Cys Met Met Ser Glu Trp Gln Gln Glu Asp Ser His Glu Tyr Phe
 435 440 445
 5 Met Ser Leu Met Ser Arg Leu Gln Glu Asp Ser Val Pro Lys Gly His
 450 455 460
 Lys Leu Ile Glu Ser Ile Ile Tyr Asp Ile Phe Gly Gly Leu Leu Lys
 465 470 475 480
 10 Gln Ile Val Thr Cys Lys Ser Cys Gly Ser Ile Ser Lys Thr Glu Gln
 485 490 495
 Pro Phe Tyr Asp Leu Ser Leu His Leu Lys Gly Lys Lys Leu Asp
 500 505 510
 15 Pro Asn Ser Asp Leu Ser Ser Asp Ser Ile Asn Gly Thr Ser Ala Thr
 515 520 525
 Thr Ser Thr Thr Thr Ser Asn Ala Ala Thr Lys Pro Ser Leu Ser Ser
 530 535 540
 Ser Ser Ser Val Asn Leu Asn Asn Gly Ser Pro Phe Ala Ala Ala Ser
 545 550 555 560

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Asp Leu Ser Ser Ala Asn Arg Arg Phe Ser Ile Glu Lys Ser Ile Lys
565 570 575

Asp Phe Phe Asn Pro Glu Leu Ile Lys Val Asp Lys Glu Gln Lys Gly
580 585 590

Tyr Val Cys Glu Lys Cys His Lys Thr Thr Asn Ala Val Lys His Ser
595 600 605

Ser Ile Leu Arg Ala Pro Glu Thr Leu Leu Val His Leu Lys Lys Phe
610 615 620

Arg Phe Asn Gly Thr Ser Ser Ser Lys Met Lys Gln Ala Val Ser Tyr
625 630 635 640

Pro Met Phe Leu Asp Leu Thr Glu Tyr Cys Glu Ser Lys Glu Leu Pro
645 650 655

Val Lys Tyr Gln Leu Leu Ser Val Val His Glu Gly Arg Ser Leu
660 665 670

Ser Ser Gly His Tyr Ile Ala His Cys Lys Lys Gln Pro Asp Gly Ser Trp
675 680 685

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	Ala Thr Tyr Asp Asp Glu Tyr Ile Asn Ile Ile Ser Glu Arg Asp Val	
	690	695 700
5	Leu Lys Glu Pro Asn Ala Tyr Tyr Leu Leu Tyr Thr Arg Leu Thr Pro	705 710 715 720
	Lys Ser Val Pro Leu Pro Leu Ala Lys Ser Ala Met Ala Thr Gly Asn	725 730 735
10	Val Thr Ser Lys Ser Lys Gln Glu Gln Ala Val Asn Glu Pro Asn Asn	740 745 750
	Arg Pro Leu Lys Ile Asn Ser Lys Lys Asn Asn Arg Lys Lys Trp Lys	755 760 765
15	Lys Ile Lys Lys Gly Ser Ser Pro Asn Glu Lys Thr Arg Tyr Ser Trp	770 775 780
	Ile Phe Leu Phe Ser	
20		785

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10	AGAGAGTTAG AATATCTTCG TTTATCTACA TATATAAAGG GAAAGGGTTG GAATATTTTA	60
	CCGATAAGTA CTCCTCTAGA GAAACAAAAA GGGGGTTATT AAACCTTCATT CTTCTTTAAA	120
	CTTTTCAGCG ACTTCTAAAA CCTCCCTTTT GGCGTCATTT AACTAACTT CTGGTGATAT	180
15	CTTAACTCTT TTGAATTTTA ACTTCCCATC AACAAAAATG AATGCGATC TAATAGAACC	240
	AGAAAGTGGC GTTTTTTTGG CTCCTAGCAA CCCAATAAAC TCTCTCTTG GATCGCTTAG	300
20	TAAATGATAT GGCAAAATTT GTTTACTCTG AAACCTTTTC TGGGATGTCA CAGAATCTGC	360
	ACTCAGTCCA AAGACAGCAG CATATTTCTT GAGTTCCTGG TAATTGTCAC GAAATCCACA	420
	GGCCTGTCTA GTACAACCAG GCGTGCTTGC CCTGGGATAC ACMAAAAAACA CCACAACCTCT	480

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GTTATTTTCG GTGATTTTTCCT TCAAGGAGAT AGAGTCATTA TCCTTCATTTA AAAGACTCAA 540
 ATCAGGAATA GGATCGCCTA TCCTTAATTC GTTAACATCA GATGACCTAT TTGCCCTCTTG 600
 5 AACTACTGCT TGATTAGCGT TATGTTTAGG ACCCGTCTTG ATTTTCTTCT TAGGCACTTC 660
 CGGTGTCGAA ATAGGGGCCA GTTTGGACTC TTCCTCTTCC AACATTCCTT TGGATATTGC 720
 AATCCTGGTT GATCTACGTA GTGCTTCACC CATTCTATTA AGGAACTTTA ATATTACCTG 780
 10 TATAAAGCTC GTAGTATTAC TTCATCC 807

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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Met Gly Glu Ala Leu Arg Arg Ser Thr Arg Ile Ala Ile Ser Lys Arg
 1 5 10 15

Met Leu Glu Glu Glu Ser Lys Leu Ala Pro Ile Ser Thr Pro Glu
 20 25 30

Val Pro Lys Lys Lys Ile Lys Thr Gly Pro Lys His Asn Ala Asn Gln
 35 40 45

Ala Val Val Gln Glu Ala Asn Arg Ser Ser Asp Val Asn Glu Leu Glu
 50 55 60

Ile Gly Asp Pro Ile Pro Asp Leu Ser Leu Leu Asn Glu Asp Asn Asp
 65 70 75 80

Ser Ile Ser Leu Lys Lys Ile Thr Glu Asn Asn Arg Val Val Val Phe
 85 90 95

Phe Val Tyr Pro Arg Ala Ser Thr Pro Gly Cys Thr Arg Gln Ala Cys
 100 105 110

Gly Phe Arg Asp Asn Tyr Gln Glu Leu Lys Lys Tyr Ala Ala Val Phe
 115 120 125

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Gly Leu Ser Ala Asp Ser Val Thr Ser Gln Lys Lys Phe Gln Ser Lys
 130 135 140

Gln Asn Leu Pro Tyr His Leu Leu Ser Asp Pro Lys Arg Glu Phe Ile
 145 150 155 160

Gly Leu Leu Gly Ala Lys Lys Thr Pro Leu Ser Gly Ser Ile Arg Ser
 165 170 175

10 His Phe Ile Phe Val Asp Gly Lys Leu Lys Phe Lys Arg Val Lys Ile
 180 185 190

Ser Pro Glu Val Ser Val Asn Asp Ala Lys Lys Glu Val Leu Glu Val
 195 200 205

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Ala Glu Lys Phe Lys Glu Glu
 210 215

20 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2117 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10	CCCCATCCTCA GCTACACTCA CTCACTCGTC AGCCACACTC GTCGTCAACA GCTATGTCCA	60
	AGAACGAAGC CCAGGAATCT TCGCCCTCTC TGCCAGCTTC CTCTTCATCG TCGACTTCGG	120
	CATCGGCATC TCGGTCTTCC AAGAATTGCA GCAAGAACCC TTCCTCTTGG GACCCCTCAAG	180
	ATGATCTGCT GCTACGTCAT TTAAAGGAGG TCAAGAAAT GGGCTGGAAG GATATTTCGC	240
15	AATACTCCC AAACAGGACT CCTAACGCGT GTCAGTTCAG ATGGAGAAGG TTGAAGTCTG	300
	GTAAC TTGAA GTCGAACAAG ACTGCTTTGA TCGACATCAA CACCTATACG GGCCCACTCA	360
20	AGATCACCCA CGGCGATGAG ACTGCCAAGC CTCAGCAANA GCCCAGCAAG AAGGTAGAAG	420
	AAAACGTATT AACGGAAGAT ACTGCTGAGT TCACTACAAC GTCATCCATC CCGATTCCCT	480
	CCAGAAAGAC CTCGTTGCCT TCGTTTCACG CATCGATGTC ATTTTCTCAA TCTCCGTCCA	540

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ATGTGACTCC CACTACGATT GTCTCAAGG CTGCTTCTTC CATGCCGTTT GCTCCTCCCA 600
CGCTGCCGGC CGCACTCCCT CATCATCCTC ATCAACACCT ACACCACCAT CCCCATCAT 660
5 AGACTCTAAA GCCAAGGTCA AACTCTCACT CCTTCACCAA TTCTTTGAAC CAAGACCCCA 720
TCGTTGGTC TAAJGATGAG GAGAAGTATG GATTCATTCC TAAAGTATTC GTTAGATCCA 780
GAAGAAGTTC GTTTGCCTAT CCACAACAGG TAGCAATAAC CACTACTCCG TCTTCTCCAA 840
10 ACTCTTCGCA TGTCTTACTA AGCTCAAAGT CAAGAAGGGG CTCGCTTGCG AATTGGTCCA 900
GAAGATCATC GTTTAATGTT TCAAGTAACA ACACTTCAAG ACGGTCTTCA ATGATTCTTG 960
15 CACCAAATTC CGTGTCAAAC ATATTCAATG TCAACAATAG CGGCAGTAAC ACTGCTTCTA 1020
CTTCTAATAC CAACTCAAGA AGGGAATCTG TCATCAAGAA GGAATTTTCA CAAGATTAA 1080
ACAACTTAAG TAACAGTGGA GGTCTTACCT CCAACMACGG GCCCATTTTC CCCAACTCTT 1140
20 ATACCTTTAT GGATCTCCCA CATTCTTCAT CGGTGTCATC GTCATCCACT TTGCATAAGT 1200
CTAACGAGG TTCGTTTTCT GGCCATTCTA TGAAGTCATC GTGTAATCCG ACTAATCTAT 1260

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GGTCAAAGA TGAAGACGGCT TTGCTAATGG AAAACAAAAA GAGAAACCTA TCCGTTATGG 1320

AACTATCCAT TCTTTTGCCG CAGAGAACTG AGGTGGAAAT TCAATGGAGA TTAAACGCCT 1380

TGTCAAGTGA TGGGGATATG TTGTCTCCTA CACATTCCACC TCANAAAACT CTGTCCAAGA 1440

AAACTTGTCC AAGAATGTTT AAAAGTGGTT CTACCACTGA TGATGACAAA GGTAGCGACA 1500

AAGAGGACGT TATGGGTGAT GGTAGTAACG ATGATGACGA AGATAATGTA GACCCGCTGC 1560

ACCGTGCTAA ACAATCCAGT AACAAAGACTG TCTTTTCATC CAGCAGTTCC AACATATCCT 1620

CCAAAGACGT TTCACCGGAT CCGATCTTTT CACCGGATCC CGCAGATGAT TCATCGAATA 1680

CTTCTGATGC TGGTTCTAGG TGCACCATAA CCTCCGATAC CAGCTCCTCG GCTGCAACCA 1740

TGAATCGCAC CCTAATTCC AAAAACCCGC AAGATATTGC TTTGTTAAAC AACTTTCGTT 1800

CTGMAGCCAT TACTCCGAGA CCGAAGCCTT CTTCCACAC TACATCCATC ACTACCGAAA 1860

CCACCAATAA CATGATAAAC CACTCTAGTT CTACAACACTAC TACCACAAAC AACAGTCCGC 1920

TGCCAAGCAT AAACACTATC TTCAAGGATA TGCTGTGAGG GGAAAACTTA AAATGAAAAA 1980

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AAAAATAAAAA TAAAAAATAA TCAACAACAA AAAGAAAATG TGAATTTAGC GGGCTTGTTT 2040

ATTAAATTTC TATAGTTTAG CATATTTAAA AGTATAAAAAG TTTCTTTGGT TTATATGACG 2100

5 TATTCATCCA AAAAAAA 2117

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Pro Gln Leu His Ser Leu Thr Arg Gln Pro His Ser Ser Ser Thr

1 5 10 15

Ala Met Ser Lys Asn Glu Ala Gln Glu Ser Ser Pro Ser Leu Pro Ala

20 25 30

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5 Ser Ser Ser Ser Thr Ser Ala Ser Ala Ser Ala Ser Ser Lys Asn
 35 40 45
 Ser Ser Lys Asn Pro Ser Ser Trp Asp Pro Gln Asp Asp Leu Leu Leu
 50 55 60
 Arg His Leu Lys Glu Val Lys Lys Met Gly Trp Lys Asp Ile Ser Gln
 65 70 75 80
 10 Tyr Phe Pro Asn Arg Thr Pro Asn Ala Cys Gln Phe Arg Trp Arg Arg
 85 90 95
 Leu Lys Ser Gly Asn Leu Lys Ser Asn Lys Thr Ala Leu Ile Asp Ile
 100 105 110
 15 Asn Thr Tyr Thr Gly Pro Leu Lys Ile Thr His Gly Asp Glu Thr Ala
 115 120 125
 Asn Ala Gln Gln Lys Pro Ser Lys Lys Val Glu Glu Asn Val Leu Thr
 130 135 140
 Glu Asp Thr Ala Glu Phe Thr Thr Ser Ser Ile Pro Ile Pro Ser
 145 150 155 160

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Arg Lys Thr Ser Leu Pro Ser Phe His Ala Ser Met Ser Phe Ser Gln
 165 170 175
 Ser Pro Ser Asn Val Thr Pro Thr Thr Ile Val Ser Asn Ala Ala Ser
 180 185 190
 Ser Met Pro Phe Ala Pro Pro Thr Leu Pro Ala Ala Leu Pro His His
 195 200 205
 Pro His Gln His Leu His His His Pro His His Lys Thr Leu Lys Pro
 210 215 220
 Arg Ser Asn Ser His Ser Phe Thr Asn Ser Leu Asn Gln Asp Pro Ile
 225 230 235 240
 Val Arg Ser Asn Asp Glu Glu Lys Tyr Gly Phe Ile Pro Lys Val Phe
 245 250 255
 Val Arg Ser Arg Arg Ser Ser Phe Ala Tyr Pro Gln Gln Val Ala Ile
 260 265 270
 Thr Thr Thr Pro Ser Ser Pro Asn Ser Ser His Val Leu Leu Ser Ser
 275 280 285

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5 Lys Ser Arg Arg Gly Ser Leu Ala Asn Trp Ser Arg Arg Ser Ser Phe
 290 295 300
 Asn Val Ser Ser Asn Asn Thr Ser Arg Arg Ser Ser Met Ile Leu Ala
 305 310 315 320
 Pro Asn Ser Val Ser Asn Ile Phe Asn Val Asn Asn Ser Gly Ser Asn
 325 330 335
 10 Thr Ala Ser Thr Ser Ser Asn Thr Asn Ser Arg Arg Glu Ser Val Ile Lys
 340 345 350
 Lys Glu Phe Gln Gln Arg Leu Asn Asn Asn Leu Ser Asn Ser Gly Gly Pro
 355 360 365
 15 Thr Ser Asn Asn Gly Pro Ile Phe Pro Asn Ser Tyr Thr Phe Met Asp
 370 375 380
 Leu Pro His Ser Ser Ser Val Ser Ser Ser Thr Leu His Lys Ser
 385 390 395 400
 Lys Arg Gly Ser Phe Ser Gly His Ser Met Lys Ser Ser Cys Asn Pro
 405 410 415

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Thr Asn Leu Trp Ser Lys Asp Glu Asp Ala Leu Leu Met Glu Asn Lys
 420 425 430

Lys Arg Asn Leu Ser Val Met Glu Leu Ser Ile Leu Leu Pro Gln Arg
 435 440 445

Thr Glu Val Glu Ile Gln Trp Arg Leu Asn Ala Leu Ser Ser Asp Ala
 450 455 460

10 Asp Met Leu Ser Pro Thr His Ser Pro Gln Lys Thr Leu Ser Lys Lys
 465 470 475 480

Thr Cys Pro Arg Met Phe Lys Ser Gly Ser Thr Thr Asp Asp Lys
 485 490 495

15 Gly Ser Asp Lys Glu Asp Val Met Gly Asp Gly Ser Asn Asp Asp Asp
 500 505 510

20 Glu Asp Asn Val Asp Pro Leu His Arg Ala Lys Gln Ser Ser Asn Lys
 515 520 525

Thr Val Phe Ser Ser Ser Ser Asn Ile Ser Ser Lys Asp Val Ser
 530 535 540

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5 Pro Asp Pro Ile Phe Ser Pro Asp Pro Ala Asp Ser Ser Asn Thr
 545 550 555 560

 Ser Asp Ala Gly Ser Arg Cys Thr Ile Thr Ser Asp Thr Ser Ser Ser
 565 570 575

 Ala Ala Thr Met Asn Arg Thr Pro Asn Ser Lys Asn Pro Gln Asp Ile
 580 585 590

 10 Ala Leu Leu Asn Asn Phe Arg Ser Glu Ala Ile Thr Pro Arg Pro Lys
 595 600 605

 Pro Ser Ser Thr Thr Ser Ile Thr Thr Glu Thr Thr Asn Asn Met
 610 615 620

 15 Ile Asn His Ser Ser Thr Thr Thr Thr Thr Asn Asn Ser Pro Leu
 625 630 635 640

 Pro Ser Ile Asn Thr Ile Phe Lys Asp Met Leu
 645 650

(2) INFORMATION FOR SEQ ID NO:25:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 956 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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GCCACGAAGG CCGGCCTTCG TGGCCTTTTG CTCTCTTCA TTTCTTTCT TAGGGATAG 60
TTTAACTGAT TTATTTTGT TACTGTTCTC ACGAGAGGAA TAGAGTGAT TGCTATTTGT 120
ATTCATGGCA GATAAAGCTT TCATGGCTCT TTTCTTTCTT TGGGCCGTCA GTTTGACAAA 180
ATCTATATTC TCGTCATCAG AACTTGTTTC GCTATCACTA TCACTATCAC TTCCGTCATC 240
ATCATCGTCG TCGTCGTCTT CGTCATCATC ATCTTCTTCT TCTTCACTCT CTTCCTTCTTC 300
ATTTTCACTC TCTTCGCCAT CTGTTACAGC TTGGTAATCG GATGACTCTG TGCCCTCGTC 360
GTCATTGTCT ATTIGCCTTT GTATAAGTTT ACTTTTTTTT CCTTGGGAAT TATTGAAAT 420
GTTCTTGCT TTTCTTTTAA TTTTATGTGG GTTGTACTT TTGTTTTTAT CAGAATCAGA 480

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540 TACGTCACTC AAGGATGACT CAGAAAGAGTA TATAAGGCTA AATCTTCTTG GCCTCGTTGT
500 ACTCAGTGTG GGTGGTGATT GCCTGGACTT TGTATCGGAT TCGGCGCTTTT TTATGAGCCT
660 TTTAATATTT GCTGGCAGTT TACCAGAAAG TGTACTATGA TTGATCGTAC TTTTTCGAGG
720 ACTTTTTTTG CCTGCCATTT CGTTCIGTTT CCAGTTTGCC GGTGTTTTT TCCTTATTTG
780 TTTATTTGCT TCCTTGTTGA ATTTCCTTCA ATTCAACAA GCTTGAAAAAT GAATTCGTA
840 GAATGAATAT TACTAGGTTT GAAATGGTTA TTGCTTATGA TGCTCACCGA AGTTAAAAAA
900 AAATATTATA GGTGTGTCCT ATGTTAGAAT TGTGGAAAGG GAGGAATGTA ATAAATATGC
956 AGTAATTAAA TATAGCCTTT TGAAGAGTTC CTCCTTTTAA TTTCGGCCT TCGTGG

(2) INFORMATION FOR SEQ ID NO:26:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5	Met	Ala	Gly	Lys	Lys	Ser	Pro	Arg	Lys	Ser	Thr	Ile	Asn	His	Ser	Thr
	1			5					10						15	

His	Ser	Gly	Lys	Leu	Pro	Ala	Asn	Ile	Lys	Arg	Leu	Ile	Lys	Lys	Gly
		20					25						30		

10
Glu Ser Asp Thr Lys Ser Arg Gln Ser Pro Thr Leu Ser Thr Thr
35 40 45

[illegible]

Asp Val Ser Asp Ser Asp Lys Asn Lys Ser Thr Asn Pro His Lys Ile	
65	70 75 80

20 Lys Arg Lys Ala Lys Asn Ile Ser Asn Asn Ser Gln Gly Lys Lys Ser
85 90 95

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5 Lys Leu Ile Gln Arg Gln Ile Asp Asn Asp Asp Glu Gly Thr Glu Ser
 100 105 110
 Ser Asp Tyr Gln Ala Val Thr Asp Gly Glu Ser Glu Asn Glu Glu
 115 120 125
 Glu Glu Ser Glu Glu Glu Asp Asp Asp Glu Asp Asp Asp Asp
 130 135 140
 10 Asp Asp Asp Gly Ser Asp Ser Asp Ser Asp Ser Glu Thr Ser Ser
 145 150 155 160
 Asp Asp Glu Asn Ile Asp Phe Val Lys Leu Thr Ala Gln Arg Lys Lys
 165 170 175
 15 Arg Ala Met Lys Ala Leu Ser Ala Met Asn Thr Asn Ser Asn Thr Leu
 180 185 190
 Tyr Ser Ser Arg Glu Asn Ser Asn Lys Asn Lys Ser Val Lys Leu Ser
 195 200 205
 Pro Lys Lys Glu Asn Glu Glu Gln Lys Ala Thr Lys Ala Gly Leu
 210 215 220

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Arg Gly
225

5 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

15	GATCTACTTG TCTGAGATGG CCTTTGATAA AAAAATCAAT CGAGTACGCA ATAGAGGGGC	60
	AGAGACTTTG AAGAGCAAAA AAAAGAAAAA GGAAATTTTC AGTTATTGTT CCGATTTTTC	120
	CGTGTGGGGT TCGGGATGCC TAGTTGTTCC GTAATGCCAT TGAAGATAC ACTTAACTAG	180
20	GAGGCTGCTA GTACGCGACC CCTACCTACG TATTGCAAAG ATGTTTGAAG TATCAACGGG	240
	TGTAGAACTT TGCAATCAAG CMAAAGCTAG ATAGTTCCAT TATGAATTGT GACGATGTTA	300

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360 CCCGTAAGTC CTACTACATC TCTTTATACG GATTGAAATC TCTAAAGGTT GCCCTGCCCG
420 TCGTTTCTTT TTCGTTGGAA TTCCTTTTTT TTTTTCATCT CATCACTAAA
480 TTGATTTAAA GTACAACCTAG GGAAGAAGAGA CTAGATAATA GTGCTTTAC ACGTTTGAC
540 GTTAGCTTT TACGGCTCTT TAATTGACTT GCTGTAAGTA TTTGTATAAT CATGGTAAT
600 ATTTGAATAC ATTCGAAACA CTGCTACAA GAAATTAAAA GGAGGAACTC TTCAAAAAGGC
660 TATATTTAAT TACTGCTTAT TTATTACATT CCTCCCTTTC CACAATTCTA ACATAGGACA
720 AACCTATAAT ATTTTCTTAA CTTCGGTGAG CATCATTAAGC AATAACCATT TCAACACATAG
780 TAATATTTCAT TCTACGAAAT TCATTTTCAA GCTTGTGTGA ATTGAAGGAA ATTCAACAAG
840 GAAGCAAATA AACAAATAAG GAAAAAACA CCGGCAAACT GGAAACAGAA CGAAATGGCA
900 GGCAAAAAA GTCTCGAAA AAGTACGATC AATCATAGTA CACATTCTGG TAAACTGCCA
960 GCAATATTA AAAGGCTCAT AAAAAAGGC GAATCCGATA CAAAGTCCAG GCAATCACCA
1020 CCCACACTGA GTACAACGAG GCCAAGAAGA TTTAGCCTTA TATACTCTTC TGAGTCATCC

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TTGAGTGACG TATCTGATTC TGATAAAAAC AAAAGTACAA ACCCACATAA AATTAAAAAGA 1080

AAAGCAAAGA ACATTTTCANA TAATTCCCAA GGAAAAAANA GTAACTTAT ACAAAGGCAA 1140

5 ATAGACAATG ACGACGAGGG CACAGAGTCA TCCGATTACC AAGCTGTAAC AGATGGCGAA 1200

GAGAGTGAAA ATGAAGAAGA AGAGAGTGAA GAAGAAGAAG AAGATGATGA CGAAGACGAC 1260

GACGACGATG ATGATGACGG AAGTGATAGT GATAGTGATA GCGAAACAAG TTCTGATGAC 1320

10 GAGAAATATAG ATTTTGTCAA ACTGACGGCC CAAAGAAAAGA AAAGAGCCAT GAAAGCTTTA 1380

TCTGCCATGA ATACAAATAG CAATACACTC TATTCCTCTC GTGAGAACAG TAACAAAAAT 1440

15 AAATCAGTTA AACTATCCCC TAAGAAAGAA AATGAAGAAG AGCAGAAAAGA AGAAAAAGAA 1500

AAAGAGAAAAG AAGAGCAACA AAAACAACAA GAATCAACA AAAAAGAAGT AAACGGTTCA 1560

GGCACTACTA CTACACAACA GGCCTATCG TTTAAATTCA AAAAGAGGA CGACGGCATT 1620

20 AGTTTGGTA ATGGTAATGA AGGCTATAAC GAGGATATAG GTGAAGAAGT CTTGGATTTA 1680

AAAAACAAAG AGAACAATGG TAATGAAGAA GATAAACTGG ATTCTAAGGT GATGTTAGGT 1740

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1800 AACACGATG AGTTACGATT TCCCAATAATT TCAGAGTCAG ATGAATCTGA ATATGATATT
1860 GACCAGGATG CGTACTTTGA CGTGATTAAAC AATGAAGATT CTCATGGAGA AATTGGTACA
1920 5 GATCTTGAAA CGGGGGAAGA CGATCTTCCC ATATTGGAAG AAGAAGAACA AAACATTGTT
1980 TCTGAGCTAC AAAATGACGA CGAACTCTCA TTCGATGGTA GTATACACGA AGAAGGGTCT
2040 GATCCTGTAG AAGATGCTGA AAATAAATTT TTGCAAAATG AATACAATCA AGAAAAACGGA
2100 10 TATGATGAAG AAGATGACGA AGAAGATGAA ATAATGTCTG ATTTTGATAT GCCGTTTTAT
2160 GAAGATCCTA AATTGCAAA TCTTTATTAT TATGGCGATG GTTCAGAGCC AAAGCTATCC
2220 15 TTGAGTACAT CTTTACCGTT AATGCTAAAT GATGAAAAAC TATCTAAACT AAAAAAGAAA
2280 GAGGCCAAA AACGGGAACA GGAAGAAAGG AAACAAAAGAC GAAAGCTCTA TAAAAAGACG
2340 CAAAAACCTA GTACGAGAAC AACCTCCAAT GTGGACAATG ATGAGTATAT TTTCATGTT
2400 TTTTTTCAAT CAGATGATGA AAATAGTGGC CATAAGAGCA AGAAAGGCAG GCATAAATCG
2460 GCCAAAAGTC ATATTGAACA TAAGAAATAA GGCTCGAATT TGATAAAATC CAATGATGAT

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CTGGAACCAT CCACTCAATAG TACGGTCCTG AATTCGGGA AATATGATTC TTCTGACGAT 2520

GAATATGATA ACATTTTGTGTT GGATGTTGCC CATATGCCTT CAGATGATGA ATGCAGTGAA 2580

5 TCTGAACCGT CCCACGAATGC TGACACGGAT GAAGAAATTGA GGGCACTAGA TTCAGATAGC 2640

TTAGACATTG GCACAGAACT GGACGACGAT TACGAAGACG ACGACGATGA TTCCAGCGTG 2700

ACAAATGTGT TCATAGACAT CGATGATTTA GATCCAGACT CTTTTTACTT TCATTACGAC 2760

10

AGCGATGGAT CTTCCCTCTTT GATAAGTTCT AACTCAGACA AAGAAAATTTC TGATGGATCC 2820

AAAGATTGCA AACATGATCT CTTAGAGACT GTTGTGTACG TTGATGACGA ATCCACAGAT 2880

15 GAAGATGATA ACCTACCGCC CCCAAGTTCA AGGTCAAAAA ACATTGGCTC AAAAGCAAAG 2940

GAAATCGTAA GTTCAAATGT TGTTGGATTA CGTCCACCAA AATTGGGTAC TTGGGAGACG 3000

GACAAACAAC CTTTTAGTAT TATTGATGGT CTGTCTACTA AATCATTATA CGCCTTAATC 3060

20

CAAGAACATC AACAGCTTCG CGAGCAACAT CAAAGGGCTC AAACCCACAGA TGTAAAAAGA 3120

GAGGGAAGCT CTAATGGCAA TAACGGTGAC GAATTGACAC TCAATGAGCT GCTAAACATG 3180

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AGTGAATTGG AGGATGATTC ACCATCCCAC ACAGACGATA TGGAGAACA TTACAATGAT 3240

GCAATTAATA GCAAMGCAC AAATGGCCAT GCTGCAGATT GGTATGAAGT TCCTAAGGTT 3300

5 CCATTATCTG CATTTAGAAA TAAGGGTATT AATGCCCTATG AAGAAGATGA GTACATGATA 3360

CCAGCAAATT CTAACAGAAA AGTTCCCATT GGCTATATTG GTAATGAAAG AACAAGAAAG 3420

AAGATTGATA AGATGAAAGA GCTACAACGG AAAAAAACTG AAAAAAAAAG GCAGTTAAAG 3480

AAAAAAAAAGA AGCTTCTTAA AATAAGAAAG CAAAGACAAA AGGCAATAAA GGAGCAAGAA 3540

ACTATGAATT TACAAITGGG AATCAATGGC CATGAGATCA TCGGTAACAA TAACAGCCAT 3600

15 AGCGACATAA ATACCGGTAC CGATTTTACA ACCAATGAAA ATACCCCTAT GAATGAACTT 3660

CCCTCTCAG CACCTGAAGA TCGGTCATTA ATACCTCATA ATTCTGATCT TGCCGTGGAC 3720

AGCAATACAA GGAAAAATTC AACAAAAAAGT GTTGGTTTAG ATGAAATTC TGAATTTTG 3780

20 GGCAAGATG AAAATGACTT ACTGTCTGTA GGTGATATTA ACGGTTATGA TGCACAAGAA 3840

GGTCATGTGA TCGAAGATAC TGACGCCCGAT ATCCTAGCAT CGTTAACCGC TCCTGTGCAA 3900

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3960
TTGACAATA CATTAGCCA TGAAAATAGT AATTCATGT GGAGAAGAAG GCAAAGTATG
4020
GTGGAAGCAG CGGCTGAAA TCTTCGTTTC ACTAAAAATG GTTTATTTAG TGAGAGTGCA
4080
5 TTGGCAGATA TCGAAGGAAT TATGGGCAAT GATGTTAACC ATTCAATCGA ATTCAAATGAC
4140
GTCTTACAAT GAGCTATTTT GCATTTTTTT ATGGTTACTA CAATCAAATC ACCTTTCGTT
4200
TACAATATCA TCATCAGTAT GTGACTTTGC CTTATTCTAC TCTGAATTTT GCTTTATCGT
4260
10 TGGTTGAAA GAATTACATG TTATTTTTTT ACTTATATAT GCATATTTT ATAGAAAAAC
4320
ACAATCAATA TTTTTTTTAC TGGTATAATC CGTCCAATCA GACGTATAAA AGTAAATAAG
4380
15 CCTCAGCAAC CCCATTGTAT GGATTGCCTT ACTCTTCGAC TCTAGTTGAG ATGATAACCT
4440
CATCCACTCT TCTGGCGATT AAGATGGAGC TTCTTAATAT ATCCGTGTAA AGCGACTGAA
4500
AATTTTCTGA AAAATTTCAGC TCATCGCTCT CAGATATAAT AGCGGTATGG CATTAAAGGT
4560
20 GTGAACCAAC AACATAGTAC TCTCAACGGT AGTAAGCCAT ACTACGTACA ATATGGATCT
4599
GAAAACCTCA TATAAAGGTA TATCGTTAAA CCCTATTTA

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ala	Gly	Lys	Lys	Ser	Pro	Arg	Lys	Ser	Thr	Ile	Asn	His	Ser	Thr
1				5					10					15	

15	His Ser Gly Lys Leu Pro Ala Asn Ile Lys Arg Leu Ile Lys Lys Gly	
		20
		25
		30

Glu Ser Asp Thr Lys Ser Arg Gln Ser Pro Pro Thr Leu Ser Thr Thr
35 40 45

20

Arg Pro Arg Arg Phe Ser Leu Ile Tyr Ser Ser Glu Ser Ser Leu Ser

50 55 60

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Asp Val Ser Asp Ser Asp Lys Asn Lys Ser Thr Asn Pro His Lys Ile
65 70 75 80

Lys Arg Lys Ala Lys Asn Ile Ser Asn Asn Ser Gln Gly Lys Lys Ser
85 90 95

5

Lys Leu Ile Gln Arg Gln Ile Asp Asn Asp Asp Glu Gly Thr Glu Ser
100 105 110

Ser Asp Tyr Gln Ala Val Thr Asp Gly Glu Glu Ser Glu Asn Glu Glu
115 120 125

10

Glu Glu Ser Glu Glu Glu Glu Asp Asp Asp Glu Asp Asp Asp Asp
130 135 140

15

Asp Asp Asp Asp Gly Ser Asp Ser Asp Ser Asp Ser Glu Thr Ser Ser
145 150 155 160

Asp Asp Glu Asn Ile Asp Phe Val Lys Leu Thr Ala Gln Arg Lys Lys
165 170 175

20

Arg Ala Met Lys Ala Leu Ser Ala Met Asn Thr Asn Ser Asn Thr Leu
180 185 190

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Tyr Ser Ser Arg Glu Asn Ser Asn Lys Asn Lys Ser Val Lys Leu Ser
 195 200 205
 Pro Lys Lys Glu Asn Glu Glu Gln Lys Glu Glu Lys Glu Lys Glu
 210 215 220
 Lys Glu Glu Gln Lys Lys Gln Glu Ser Asn Lys Lys Glu Val Asn
 225 230 235 240
 Gly Ser Gly Thr Thr Thr Gln Gln Ala Leu Ser Phe Lys Phe Lys
 245 250 255
 Lys Glu Asp Asp Gly Ile Ser Phe Gly Asn Gly Asn Glu Gly Tyr Asn
 260 265 270
 Glu Asp Ile Gly Glu Glu Val Leu Asp Leu Lys Asn Lys Glu Asn Asn
 275 280 285
 Gly Asn Glu Glu Asp Lys Leu Asp Ser Lys Val Met Leu Gly Asn Asn
 290 295 300
 Asp Glu Leu Arg Phe Pro Asn Ile Ser Glu Ser Asp Glu Ser Glu Tyr
 305 310 315 320

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Asp Ile Asp Gln Asp Ala Tyr Phe Asp Val Ile Asn Asn Glu Asp Ser
325 330 335

His Gly Glu Ile Gly Thr Asp Leu Glu Thr Gly Glu Asp Asp Leu Pro
340 345 350

Ile Leu Glu Glu Glu Gln Asn Ile Val Ser Glu Leu Gln Asn Asp
355 360 365

Asp Glu Leu Ser Phe Asp Gly Ser Ile His Glu Glu Gly Ser Asp Pro
370 375 380

Val Glu Asp Ala Glu Asn Lys Phe Leu Gln Asn Glu Tyr Asn Gln Glu
385 390 395 400

Asn Gly Tyr Asp Glu Glu Asp Asp Glu Glu Asp Glu Ile Met Ser Asp
405 410 415

Phe Asp Met Pro Phe Tyr Glu Asp Pro Lys Phe Ala Asn Leu Tyr Tyr
420 425 430

Tyr Gly Asp Gly Ser Glu Pro Lys Leu Ser Leu Ser Thr Ser Leu Pro
435 440 445

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Asp Asp Glu Cys Ser Glu Ser Glu Thr Ser His Asp Ala Asp Thr Asp
580 585 590

Glu Glu Leu Arg Ala Leu Asp Ser Asp Ser Leu Asp Ile Gly Thr Glu
595 600 605

Leu Asp Asp Asp Tyr Glu Asp Asp Asp Asp Ser Ser Val Thr Asn
610 615 620

Val Phe Ile Asp Ile Asp Asp Leu Asp Pro Asp Ser Phe Tyr Phe His
625 630 635 640

Tyr Asp Ser Asp Gly Ser Ser Ser Leu Ile Ser Ser Asn Ser Asp Lys
645 650 655

Glu Asn Ser Asp Gly Ser Lys Asp Cys Lys His Asp Leu Leu Glu Thr
660 665 670

Val Val Tyr Val Asp Asp Glu Ser Thr Asp Glu Asp Asp Asn Leu Pro
675 680 685

Pro Pro Ser Ser Arg Ser Lys Asn Ile Gly Ser Lys Ala Lys Glu Ile
690 695 700

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Val Ser Ser Asn Val Val Gly Leu Arg Pro Pro Lys Leu Gly Thr Trp
 705 710 715 720

Glu Thr Asp Asn Lys Pro Phe Ser Ile Ile Asp Gly Leu Ser Thr Lys
 725 730 735

Ser Leu Tyr Ala Leu Ile Gln Glu His Gln Gln Leu Arg Glu Gln His
 740 745 750

Gln Arg Ala Gln Thr Pro Asp Val Lys Arg Glu Gly Ser Ser Asn Gly
 755 760 765

Asn Asn Gly Asp Glu Leu Thr Leu Asn Glu Leu Leu Asn Met Ser Glu
 770 775 780

Leu Glu Asp Asp Ser Pro Ser His Thr Asp Asp Met Glu Asn Asn Tyr
 785 790 795 800

Asn Asp Ala Ile Asn Ser Lys Ser Thr Asn Gly His Ala Ala Asp Trp
 805 810 815

Tyr Glu Val Pro Lys Val Pro Leu Ser Ala Phe Arg Asn Lys Gly Ile
 820 825 830

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Asn Ala Tyr Glu Glu Asp Glu Tyr Met Ile Pro Ala Asn Ser Asn Arg
835 840 845

Lys Val Pro Ile Gly Tyr Ile Gly Asn Glu Arg Thr Arg Lys Lys Ile
850 855 860

Asp Lys Met Lys Glu Leu Gln Arg Lys Lys Thr Glu Lys Lys Arg Gln
865 870 875 880

10 Leu Lys Lys Lys Lys Leu Leu Lys Ile Arg Lys Lys Gln Arg Gln Lys
885 890 895

Ala Ile Lys Glu Gln Glu Thr Met Asn Leu Gln Leu Gly Ile Asn Gly
900 905 910

15

His Glu Ile Ile Gly Asn Asn Asn Ser His Ser Asp Ile Asn Thr Gly
915 920 925

Thr Asp Phe Thr Thr Asn Glu Asn Thr Pro Met Asn Glu Leu Pro Ser
930 935 940

His Ala Pro Glu Asp Ala Ser Leu Ile Pro His Asn Ser Asp Leu Ala
945 950 955 960

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Val Asp Ser Asn Thr Arg Lys Asn Ser Thr Lys Ser Val Gly Leu Asp
 965 970 975

Glu Ile His Glu Ile Leu Gly Lys Asp Glu Asn Asp Leu Leu Ser Val
 980 985 990

Gly Asp Ile Asn Gly Tyr Asp Ala Gln Glu Gly His Val Ile Glu Asp
 995 1000 1005

Thr Asp Ala Asp Ile Leu Ala Ser Leu Thr Thr Ala Pro Val Gln Phe Asp
 1010 1015 1020

Asn Thr Leu Ser His Glu Asn Ser Asn Ser Met Trp Arg Arg Arg Gln
 1025 1030 1035 1040

Ser Met Val Glu Ala Ala Glu Asn Leu Arg Phe Thr Lys Asn Gly
 1045 1050 1055

Leu Phe Ser Glu Ser Ala Leu Ala Asp Ile Glu Gly Ile Met Gly Asn
 1060 1065 1070

Asp Val Asn His Ser Phe Glu Phe Asn Asp Val Leu Gln
 1075 1080 1085

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5	ATCAAGGAGG TCACCAGTAA TTGTGCGCTT TGGTTACATT TTGTTGTACA GTAATGGGCG	50
10	ATCAAGAAAG TATATCAAAT AATAACTCAG ACTCATTTCAT TATGTCGTCC CCCAACTTAG	120
15	ACTCTCAGGA ATCTTCAATA TCACCTATTG ATGAGAAGAA AGGCACCGAT ATGCAAAACCA	180
	AGTCGCTTTC AAGCTATTCT AAAGGTACGC TTCTCTCTAA GCAAGTACAA AATTATTAG	240
20	AAGAAGCTAA TAAATACGAT CCAATATAAG GGTCACTCTT ACCTCGAGGA TTTTAAAGAG	300
	ATAGAAACAC CAAGGGTAAG GATAATGGGT TGGTTCCGCT GGTGGAGAAG GTTATACCTC	360

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CCATTACAA GAAAGCCAAAT AATAGAAACA CAAGGAAGAA GTCATCTACC ACCACGAAGA 420

AGGATGTAAA GAAGCCAAAA GCTGC AAAAG TAAAGGAAA AATGGCAGG ACTAACCATA 480

5 AACATACCCC AATTTCAAAG CAAGAAATAG ATACTGCACG AGAAAAAAG CCATTGAAAA 540

AAGGTCGGGC AAACAAGAAG AATGATCGCG ATAGTCCTTC ATCAACATTT GTTGATTGGA 600

ATGGCCCGTG TCTACGGTTA CAATATCCAT TATTTGACAT AGAGTACTTA AGATCACATG 660

10 AAATATATTC TGGAACTCCT ATACAATCCA TTAGTTTAAG AACAAATTCT CCACAGCCAA 720

CGAGCTTGAC ATCAGATAAC GACACTTCCT CAGTAACGAC AGCAAAGTTG CAGAGTATTT 780

15 TATTTTCAA TTATATGGAA GAGTACAAA TCGACTTCAA AAGGTCAACA GCCATTATATA 840

ATCCAATGAG TGAAATTGGT AAATTAATTG AATACAGCTG CCTGGTCITT TTACCTTCAC 900

CTTATGCTGA ACAATIGAAG GAAACTATAC TACCGGACCT AAATGCATCA TTTGATAACT 960

20 CTGACACGAA AGGTTTCGTC AATGCTATAA ATTATATACA CAAATGATT CGTGAAATTC 1020

CTAGGCAAG AATAATTGAC CATTTAGAAA CAATTGATAA AATTCCTCGT TCATTTCATTC 1080

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ATGACTTCTT GCATATCGTC TATACCAGGA GTATCCATCC GCAGGCGAAT AAATTGAAAC 1140
ATTACAAAGC ATTCAGCAAT TATGTTTATG GAGAACTTTT GCCCAATTTC CTATCTGATG 1200
5 TATATCAACA ATGCCAGTTG AAGAAGGGTG ACACTTTTCAT GGATCTCGGT TCGGGAGTAG 1260
GTAATTGCGT AGTACAAGCT GCGTTGGAAT GTGGATGTGC ATTAAGCTTC GGATGTGAAA 1320
TCATGGATGA TGCTAGCGAT TTAACATATAC TGCAGTACGA GGAACATAAG AAGAGGTGTA 1380
10 AGTTATATGG GATGCGTTTG AACAAACGTGG AGTTTTCATT GAAGAAAAGC TTTGTGGACA 1440
ATAACAGGGT CGCTGAACTA ATTCCTCAGT GCGATGTTAT CCTCGTAAAT AATTTTAT 1500
15 TTGATGAAGA TTTGAATAAA AAAGTCGAAA AGATACTACA AACGGCAAAA GTTGGATGTA 1560
AGATCATAAG TTTGAAAAGT TTAAGAAGCC TCACCTATCA GATCAACTTC TACAATGTTG 1620
AGAACATCTT CAATAGATTA AAGGTGCAAA GGTATGATCT TAAGGAGGAT AGTGTTTCAT 1680
20 GGACGCATAG TGGCGGAGAG TATTATATAT CAACAGTGTAT GGAGGATGTG GACGAAAGTT 1740
TATTACGCCC TGCTGCAAGA GGTAGGAGGA ACAGAGGTAC GCCGGTGAAG TATACCAGAT 1800

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GAGGCACTTT GAACGGC"TTT TAACGATGAG TATGAATAAC TAAGTAGAAA TAACATGTAC 1860

ACAAAGTGTA CTTATAAAAA TC 1882

5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

15

CAAAATTGGG AGAAACATA CTCAAAGTGAG TACTCATTTT GTGCAAGCAA ACACTGACAA 60

TTGAAGAGAT CGTCAGGATG CCCGGAACGC CACAGAAGAA CAAGAGGTCT GCGAGTATAT 120

CTGTTTCACC TGCGAAGAAG ACAGAGGAAA AAGAAATAAT ACAAATGAT TCAAAGGCGA 180

TATTATCTAA GCMAACTAAG AGGAAAAAAA AGTATGCTTT TGCTCCTATA AATAACTTAA 240

20

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ATGGGAAGAA CACCAAGGTA TCCAATGCAA GTGTCCTAAA GTCAATAGCC GTTTCACAAG 300

TACGAAATAC ATCAAGNACA AAAGATATAA ACAAGCAGT TAGCAAGAGC GTAAAGCAAT 360

5 TACCAAAATTC ACAAGTTAAA CCGAAACGGG AAATGTCTAA TTTGAGTAGG CATCACGATT 420

TCACTCNAGA CGAGGACGGC CCCATGGAAG AAGTAATATG GAAATATTCA CCTTTACAAC 480

GAGATATGTC CGACAAAACA ACAAGCGCTG CCGAATACTC TGATGACTAC GAAAGATGTCC 540

10 AAAATCCCCTC TTCTACACCT ATAGTCCCTA ATCGACTGAA AACTGTTCTT AGTTTCACAA 600

ATATCCAAGT ACCCAACGCT GACGTAAATC AACTCATTCA AGAAAAATGGA AATGAGCAAG 660

15 TCGGTCCTAA ACCAGCAGAA ATATCTACCA GGGAGTCTCT CCGTAATATA GATGATATTTC 720

TCGATGATAT AGAGGGCGAT TTAATCTATA AACCGACGAT AACGAAATTC AGCGATTTCG 780

CATCTTCACC CATCAAGGCA CCCAACGTTG AAAAAAAGC AGAGGTGAAT GCAGAAGAAG 840

20 TAGATAAAAT GGATTCAACA GGAGATAGCA ACGATGGCGA TGACTCTTTG ATAGATATTT 900

TAACTCAAAA GTATGTTGAG AAACGCAAGA GTGAGAGTCA GATAACAATT CAAGGCAACA 960

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CCAATCAAAA AAGTGGAGGC CAGGAAAGTT GTGGGAAGAA TGATAACACA AATTCGAGAG 1020

GAGAAATTGA AGATCATGAA AATGTAGACA ATCAAGCCAA AACAGGCAAT GCATTTTATG 1080

5 AGAATGAAGA AGAC 1094

(2) INFORMATION FOR SEQ ID NO:31:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGATGAAGTA ATACTACGAG CTTTATACAG GTAATATTAA AGTTCCTTAA TAGAATGGGT 60

20 GAAGCACTAC GTAGATCAAC CAGGATTGCA ATATCCAAAA GAATGTTGGA AGAGGAAGAG 120

TCCAAACTGG CCCCTATTTC GACACCGGAA GTGCCTAAGA AGAAAAATCAA GACGGGTCCT 180

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AAACATAACG CTAATCANAGC AGTAGTTTCAA GAGGCAAAATA GGTCACTCTGA TGTTAACGAA 240
TTAGAGATAG GCGATCCCTAT TCCTGATTG AGTCTTTTAA ATGAAGATAA TGA CTCTATC 300
5 TCCTTGAAGA AAATCACCGA AAATAACAGA GTTGTGGTGT TTTTGTGTGA TCCCAGGGCA 360
AGCACGCCCTG GTTGTA CTAG ACAGGCCCTGT GGATTTCGTG ACAATTACCA GGA ACTCAAG 420
AAATATGCTG CTGTCTTTGG ACTGAGTGCA GATTCTGTGA CATCCCAGAA AAAGTTTCAG 480
10 AGTAAACAAA ATTTGCCATA TCATTTACTA AGCGATCCAA AGAGAGAGTT TATTGGGTTG 540
CTAGGAGCCA AAAAAACGCC ACTTTCTGGT TCTATTAGAT CGCATTTTCAT TTTTGTGTGAT 600
GGGAAGTTAA AATTCAAAAAG AGTTAAGATA TCACCAGAAG TTAGTGTAAA TGACGCCAAA 660
AAGGAGGTTT TAGAAGTCGC TGA AAAAGTTT AAAGAAGAAT GAAGTTTAAAT AACCCCTTT 720
TTGTTTCTCT AGAGGAGTAC TTATCGGTAA AATATTCCAA ACCCTTCCCT TTATATATGT 780
20 AGATAAACGA AGATATTCTA ACTCTCT 807

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5	CCACGAAGGC CAGAAATTAA AAGGAGGAAC TCTTCAAAAG GCTATATTTA ATTACTGCAT	60
	ATTATTACA TTCCTCCCTT TCCACAATTC TAACATAGGA CAAACCTATA ATATTTTTT	120
15	TAACTTCGG TGAGCATCAT AAGCAATAAC CATTTCAAAC CTAGTAATAT TCATTCTACG	180
	AAATTCATTT TCAAGCTTGT TGAAATTGAA GGAAATTCAA CAAGGAAGCA AATAAACAAA	240
20	TAAGGAAAAA ACAACCGGCA AACTGGAAAC AGAACGAAAT GGCAGGCNAA AAAAGTCCTC	300
	GAAAAAGTAC GATCAATCAT AGTACACATT CTGGTAAACT GCCAGCAAAAT ATTAAAAAGGC	360
	TCATAAAAAA GGGCGAATCC GATACAAAGT CCAGGCAATC ACCACCCACA CTGAGTACAA	420

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CGAGGCCAAG AAGATTJAGC CTTATATACT CTTCTGAGTC ATCCTTGAGT GACGTATCTG 480
ATTCTGATAA AAACAAAAGT ACAAACCCAC ATAAAAATTAA AAGAAAAGCA AAGAACATTT 540
5 CAAATAATT CCAAGGAAAA AAAAGTAAAC TTATACAAAG GCNAAATAGAC AATGACGACG 600
AGGGCACAGA GTCATCCGAT TACCAAGCTG TAACAGATGG CGAAGAGAGT GAAAAATGAAG 660
AAGAAGAGAG TGAAGAAGAA GAAGATGATG ATGACGAAGA CGACGACGAC GATGATGATG 720
10 ACGGAAGTGA TAGTGATAGT GATAGCGAAA CAAGTTCTGA TGACGAGAAT ATAGATTTTG 780
TCAAACTGAC GGCCCAAGA AAGAAAAGAG CCAATGAAAGC TTTATCTGCC ATGAATACAA 840
15 ATAGCAATAC ACTCTATTCC TCTCGTGAGA ACAGTAACAA AAATAAATCA GTTAAACTAT 900
CCCCTAAGAA AGAAATGAA GAAGAGCAAA AGGCCACGAA GGCCGGCCTT CGTGGC 956

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CLAIMS:

1. A nucleic acid segment characterized as:
- 5
- (a) a nucleic acid segment comprising a sequence region that consists of at least 17 contiguous nucleotides that have the same sequence as, or are complementary to, 17 contiguous nucleotides of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23; or
- 10
- (b) a nucleic acid segment of from 17 to about 10,000 nucleotides in length that hybridizes to the nucleic acid segment of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or the complement thereof, under standard hybridization conditions.
- 15
- 20
2. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or the complement thereof.
- 25
3. The nucleic acid segment of claim 1, wherein the segment hybridizes to the nucleic acid segment of SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31 or SEQ ID NO:23, or the complement thereof.
- 30
4. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:1, or the
- 35

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complement thereof; or wherein the segment hybridizes to the nucleic acid segment of SEQ ID NO:1, or the complement thereof.

5

5. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:29, or the complement thereof; or wherein the segment hybridizes to
10 the nucleic acid segment of SEQ ID NO:29, or the complement thereof.

6. The nucleic acid segment of claim 1, wherein the
15 segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:30, or the complement thereof; or wherein the segment hybridizes to the nucleic acid segment of SEQ ID NO:30, or the complement thereof.

20

7. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:19, or the
25 complement thereof; or wherein the segment hybridizes to the nucleic acid segment of SEQ ID NO:19, or the complement thereof.

30 8. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:31, or the complement thereof; or wherein the segment hybridizes to the nucleic acid segment of SEQ ID NO:31, or the
35 complement thereof.

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9. The nucleic acid segment of claim 1, wherein the segment comprises a sequence region of at least 17 contiguous nucleotides from SEQ ID NO:23, or the complement thereof; or wherein the segment hybridizes to
5 the nucleic acid segment of SEQ ID NO:23, or the complement thereof.

10. The nucleic acid segment of claim 1, wherein the
10 segment comprises a sequence region of at least about 25 nucleotides; or wherein the segment is about 25 nucleotides in length.

11. The nucleic acid segment of claim 10, wherein the
15 segment comprises a sequence region of at least about 50 nucleotides; or wherein the segment is about 50 nucleotides in length.

12. The nucleic acid segment of claim 11, wherein the
20 segment comprises a sequence region of at least about 100 nucleotides; or wherein the segment is about 100 nucleotides in length.

13. The nucleic acid segment of claim 12, wherein the
25 segment comprises a sequence region of at least about 200 nucleotides; or wherein the segment is about 200
30 nucleotides in length.

14. The nucleic acid segment of claim 13, wherein the
35 segment comprises a sequence region of at least about 500 nucleotides; or wherein the segment is about 500 nucleotides in length.

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15. The nucleic acid segment of claim 14, wherein the
segment comprises a sequence region that consists of the
1301 contiguous nucleotides of SEQ ID NO:1, or the
5 complement thereof.

16. The nucleic acid segment of claim 14, wherein the
segment comprises a sequence region that consists of at
10 least about a 1000 nucleotide long contiguous sequence
from SEQ ID NO:29, or the complement thereof.

17. The nucleic acid segment of claim 16, wherein the
15 segment comprises a sequence region that consists of the
1882 contiguous nucleotides of SEQ ID NO:29, or the
complement thereof.

18. The nucleic acid segment of claim 14, wherein the
20 segment comprises a sequence region that consists of the
1094 contiguous nucleotides of SEQ ID NO:30, or the
complement thereof.

19. The nucleic acid segment of claim 14, wherein the
25 segment comprises a sequence region that consists of at
least about a 1000 nucleotide long contiguous sequence
from SEQ ID NO:29, or the complement thereof.

20. The nucleic acid segment of claim 19, wherein the
segment comprises a sequence region that consists of at
least about a 2000 nucleotide long contiguous sequence
30 from SEQ ID NO:29, or the complement thereof.

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21. The nucleic acid segment of claim 20, wherein the segment comprises a sequence region that consists of the 2434 contiguous nucleotides of SEQ ID NO:19, or the complement thereof.

5

22. The nucleic acid segment of claim 14, wherein the segment comprises a sequence region that consists of the 807 contiguous nucleotides of SEQ ID NO:31, or the complement thereof.

10

23. The nucleic acid segment of claim 14, wherein the segment comprises a sequence region that consists of at least about a 1000 nucleotide long contiguous sequence from SEQ ID NO:23, or the complement thereof.

15

24. The nucleic acid segment of claim 23, wherein the segment comprises a sequence region that consists of the 2117 contiguous nucleotides of SEQ ID NO:23, or the complement thereof.

20

25. The nucleic acid segment of claim 1, wherein the segment is up to about 10,000 basepairs in length.

25

26. The nucleic acid segment of claim 25, wherein the segment is up to about 5,000 basepairs in length.

30

27. The nucleic acid segment of claim 26, wherein the segment is up to about 1,000 basepairs in length.

35

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28. The nucleic acid segment of claim 27, wherein the segment is up to about 500 basepairs in length.

5 29. The nucleic acid segment of claim 28, wherein the segment is up to about 100 basepairs in length.

30. The nucleic acid segment of claim 1, further defined
10 as a DNA segment.

31. The nucleic acid segment of claim 1, further defined
as a RNA segment.
15

32. An isolated RNA segment of from 17 to about 1,500
nucleotides in length that comprises a non-ciliate
telomerase RNA template.
20

33. The isolated RNA segment of claim 32, comprising a
yeast telomerase RNA template.

25 34. An isolated RNA segment having the secondary
structure of the RNA segment encoded by the sequence of
SEQ ID NO:1.

30 35. An affinity column comprising a deoxyoligonucleotide
attached to a solid support, wherein the
deoxyoligonucleotide includes a GT-rich sequence
complementary to a non-ciliate telomerase RNA template
35 sequence and binds to a non-ciliate telomerase complex.

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36. A DNA segment comprising an isolated gene associated with non-ciliate telomerase.

5 37. The DNA segment of claim 36, comprising an isolated gene associated with yeast telomerase.

38. The DNA segment of claim 37, comprising an isolated
10 gene that encodes a yeast telomerase RNA template.

39. The DNA segment of claim 38, comprising an isolated gene that encodes the yeast telomerase RNA template
15 sequence CACCACACCCACACAC (SEQ ID NO:3).

40. The DNA segment of claim 39, comprising an isolated gene that includes the contiguous DNA sequence from
20 position 468 to position 483 of SEQ ID NO:1 or the contiguous DNA sequence from position 819 to position 834 of SEQ ID NO:4.

25 41. The DNA segment of claim 40, comprising an isolated gene that includes a contiguous DNA sequence from position 400 to position 500 of SEQ ID NO:1.

30 42. The DNA segment of claim 41, comprising an isolated gene that includes a contiguous DNA sequence from position 200 to position 900 of SEQ ID NO:1.

35 43. The DNA segment of claim 42, comprising an isolated gene that includes the DNA sequence of SEQ ID NO:1.

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44. The DNA segment of claim 37, comprising an isolated gene that encodes a polypeptide associated with yeast telomerase.

5

45. The DNA segment of claim 44, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

10

46. The DNA segment of claim 45, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:16.

15

47. The DNA segment of claim 46, comprising an isolated gene that encodes a polypeptide having the sequence of SEQ ID NO:16.

20

48. The DNA segment of claim 47, comprising an isolated gene that includes the contiguous DNA sequence from position 54 to position 1799 of SEQ ID NO:29.

25

49. The DNA segment of claim 45, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:18.

30

50. The DNA segment of claim 49, comprising an isolated gene that encodes a polypeptide having the sequence of SEQ ID NO:18.

35

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51. The DNA segment of claim 50, comprising an isolated gene that includes the contiguous DNA sequence from position 78 to position 1094 of SEQ ID NO:30.

5

52. The DNA segment of claim 45, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:20.

10

53. The DNA segment of claim 52, comprising an isolated gene that encodes a polypeptide having the sequence of SEQ ID NO:20.

15

54. The DNA segment of claim 53, comprising an isolated gene that includes the contiguous DNA sequence from position 2 to position 2368 of SEQ ID NO:19.

20

55. The DNA segment of claim 45, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:22.

25

56. The DNA segment of claim 55, comprising an isolated gene that encodes a polypeptide having the sequence of SEQ ID NO:22.

30

57. The DNA segment of claim 56, comprising an isolated gene that includes the contiguous DNA sequence from position 55 to position 699 of SEQ ID NO:31.

35

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58. The DNA segment of claim 45, comprising an isolated gene that encodes a polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:24.

5

59. The DNA segment of claim 58, comprising an isolated gene that encodes a polypeptide having the sequence of SEQ ID NO:24.

10

60. The DNA segment of claim 59, comprising an isolated gene that includes the contiguous DNA sequence from position 3 to position 1955 of SEQ ID NO:23.

15

61. The DNA segment of claim 37, wherein the isolated gene is positioned under the control of a promoter.

20

62. The DNA segment of claim 61, positioned under the control of a recombinant promoter.

25

63. The DNA segment of claim 62, further defined as a recombinant vector.

30

64. A recombinant host cell incorporating a DNA segment that comprises an isolated gene associated with non-ciliate telomerase.

35

65. The recombinant host cell of claim 64, further defined as a prokaryotic host cell.

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66. The recombinant host cell of claim 64, further defined as a eukaryotic host cell.

5 67. The recombinant host cell of claim 66, further defined as a yeast cell.

68. The recombinant host cell of claim 66, further
10 defined as a mammalian cell.

69. The recombinant host cell of claim 64, wherein the host cell expresses the DNA segment to produce a
15 telomerase RNA template or a polypeptide associated with telomerase.

70. A method of using a DNA segment that comprises an isolated gene associated with non-ciliate telomerase, the
20 method comprising the steps of:

- 25 (a) preparing a recombinant vector in which a non-ciliate telomerase-associated gene is positioned under the control of a promoter;
- (b) introducing said recombinant vector into a recombinant host cell;
- 30 (c) culturing the recombinant host cell under conditions effective to allow expression of the telomerase-associated gene; and
- (d) collecting the expressed gene product.

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71. A recombinant gene product prepared by expressing a non-ciliate telomerase-associated gene in a recombinant host cell and purifying the expressed gene product away from total recombinant host cell components.

5

72. The gene product of claim 71, wherein the gene product is a telomerase RNA template.

10

73. The gene product of claim 71, wherein the gene product is a polypeptide associated with telomerase.

15

74. A method for detecting a non-ciliate telomerase-associated gene in a sample, the method comprising the steps of:

20

(a) obtaining sample nucleic acids from a sample suspected of containing a non-ciliate telomerase-associated gene;

25

(b) contacting said sample nucleic acids with a nucleic acid segment that includes at least a 17 nucleotide long contiguous sequence from SEQ ID NO:1, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:19, SEQ ID NO:31, SEQ ID NO:23, or the complement thereof, under conditions effective to allow hybridization of substantially complementary nucleic acids; and

30

(c) detecting the hybridized complementary nucleic acids thus formed.

35

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75. The method of claim 74, wherein the sample nucleic acids are obtained from a sample suspected of containing a tumor cell.

5

76. The method of claim 74, wherein the sample nucleic acids are obtained from a sample suspected of containing a pathogen.

10

77. The method of claim 74, wherein the sample nucleic acids are obtained from a sample suspected of containing a sperm cell or an egg cell.

15

78. A polypeptide composition, free from cell components, comprising a purified non-ciliate telomerase-associated polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

20

79. An antibody that binds to a non-ciliate telomerase-associated polypeptide that includes a contiguous amino acid sequence from SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

25

80. A method for identifying a gene associated with a non-ciliate telomerase, the method comprising the steps of:

30

(a) preparing a cell containing a chromosome that contains a genetic marker located proximal to a telomere, the telomere repressing the expression of the marker;

35

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(b) contacting said cell with a composition
comprising a candidate gene; and

5 (c) identifying a gene that allows expression of
the marker.

10 81. The method of claim 80, wherein said cell is a
Drosophila melanogaster cell.

82. The method of claim 80, wherein said cell is a human
cell.

15 83. The method of claim 82, wherein said cell is a human
sperm cell or a human egg cell.

20 84. The method of claim 82, wherein said cell is a human
cancer cell.

25 85. The method of claim 80, wherein said cell is a yeast
cell.

30 86. The method of claim 85, wherein said genetic marker
is *HIS3*, *TRP1*, *LYS2*, *LEU2*, *CAN1*, *ADE2* or *URA3*.

87. The method of claim 86, wherein said genetic markers
is *ADE2* or *URA3*.

35

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88. The method of claim 85, wherein said cell contains two distinct genetic markers, each located on a distinct chromosome.

5

89. The method of claim 88, wherein said genetic markers are *ADE2* and *URA3*.

10 90. The method of claim 80, wherein said candidate gene is a mutant or truncated gene.

15 91. The method of claim 80, wherein said candidate gene is a wild type gene.

92. A gene identified by the method of claim 80.

20

93. The gene of claim 92, the gene having the physical and functional characteristics of *TLC1*.

25 94. The gene of claim 92, the gene having the physical and functional characteristics of *STR1*.

30 95. The gene of claim 92, the gene having the physical and functional characteristics of *STR3*.

96. The gene of claim 92, the gene having the physical and functional characteristics of *STR4*.

35

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97. The gene of claim 92, the gene having the physical and functional characteristics of *STR5*.

5 98. The gene of claim 92, the gene having the physical and functional characteristics of *STR6*.

99. A method for identifying a human telomerase-associated gene, the method comprising the steps of:

15 (a) preparing a yeast cell containing a chromosome that contains a genetic marker located proximal to a telomere, the telomere repressing the expression of the marker;

(b) contacting said cell with a composition comprising a candidate human gene; and

20 (c) identifying a human gene that allows expression of the marker.

100. A method for identifying a candidate substance that binds to a non-ciliate telomerase component, the method comprising the steps of:

30 (a) preparing an isolated non-ciliate telomerase component;

(b) contacting said isolated telomerase component with a composition comprising a candidate substance under conditions effective to allow binding; and

35

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- (c) detecting the presence of a telomerase
component-candidate substance bound complex.

- 5 101. The method of claim 100, wherein said isolated
telomerase component is an RNA segment comprising a non-
ciliate telomerase RNA template.
- 10 102. The method of claim 100, wherein said isolated
telomerase component is a DNA segment encoding a non-
ciliate telomerase-associated polypeptide.
- 15 103. The method of claim 100, wherein said isolated
telomerase component is a polypeptide associated with
non-ciliate telomerase.
- 20 104. A component that binds to a non-ciliate telomerase
component.
- 25 105. The component of claim 104, identified by the method
of claim 100.
- 30 106. The component of claim 104, wherein the component is
a nucleic acid segment.
107. The component of claim 106, wherein the nucleic acid
segment is a human nucleic acid segment.

35

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108. The component of claim 106, wherein the nucleic acid segment hybridizes to a yeast telomerase nucleic acid segment under standard low stringency hybridization conditions.

5

109. The component of claim 106, wherein the nucleic acid segment hybridizes to a yeast telomerase nucleic acid segment under standard high stringency hybridization conditions.

10

110. The component of claim 104, wherein the component is a protein or polypeptide.

15

111. A method for identifying a candidate substance that modifies telomerase activity, the method comprising the steps of:

20

(a) preparing a cell containing a chromosome that contains a genetic marker located near a telomere, the telomere capable of repressing the expression of the marker;

25

(b) contacting said cell with a composition comprising a candidate substance; and

30

(c) identifying a candidate substance that allows expression of the marker or that further represses the expression of the marker.

112. The method of claim 111, further defined as a method for identifying a candidate substance that inhibits telomerase activity, the method comprising the steps of:

35

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- 5
- (a) preparing a cell containing a chromosome that contains a genetic marker located proximal to a telomere, the telomere significantly repressing the expression of the marker;
 - (b) contacting said cell with a composition comprising a candidate inhibitory substance; and
 - 10 (c) identifying a candidate inhibitory substance that allows expression of the marker.

15 113. The method of claim 111, further defined as a method for identifying a candidate substance that stimulates telomerase activity, the method comprising the steps of:

- 20
- (a) preparing a cell containing a chromosome that contains a genetic marker located in the vicinity of a telomere, the telomere not significantly repressing the expression of the marker;
 - 25 (b) contacting said cell with a composition comprising a candidate substance; and
 - (c) identifying a candidate stimulatory substance that represses or further represses the expression of the marker.

30

114. A method for modifying the replicative capacity of a cell, comprising contacting a telomerase-containing cell with an amount of a candidate substance effective to
35 modify telomerase activity.

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115. The method of claim 114, further defined as a method
for inhibiting the replication of a cell, comprising
contacting a telomerase-containing cell with an amount of
an inhibitory substance effective to inhibit telomerase
5 activity.

116. The method of claim 115, wherein said telomerase-
containing cell is a tumor cell.
10

117. The method of claim 115, wherein said telomerase-
containing cell is a pathogenic cell.

118. The method of claim 114, further defined as a method
for promoting the replication of a cell, comprising
contacting a telomerase-containing cell with an amount of
a stimulatory substance effective to promote telomerase
20 activity.

119. The method of claim 118, wherein said telomerase-
containing cell is a sperm cell.
25

120. The method of claim 118, wherein said telomerase-
containing cell is an egg cell.

121. The use of a substance that inhibits telomerase
activity in the preparation of a medicament for use in
killing pathogenic or tumor cells, said substance being
identified by a method comprising the steps of:
35

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- 5
- (a) preparing a cell containing a chromosome that contains a genetic marker located proximal to a telomere, the telomere significantly repressing the expression of the marker;
 - (b) contacting said cell with a composition comprising a candidate inhibitory substance; and
 - 10 (c) identifying a candidate inhibitory substance that allows expression of the marker.

15 122. The use of a substance that stimulates telomerase activity in the preparation of a medicament for use in promoting the replication of a sperm or egg cell, said substance being identified by a method comprising the steps of:

- 20
- (a) preparing a cell containing a chromosome that contains a genetic marker located in the vicinity of a telomere, the telomere not significantly repressing the expression of the marker;
 - 25 (b) contacting said cell with a composition comprising a candidate substance; and
 - 30 (c) identifying a candidate stimulatory substance that represses or further represses the expression of the marker.

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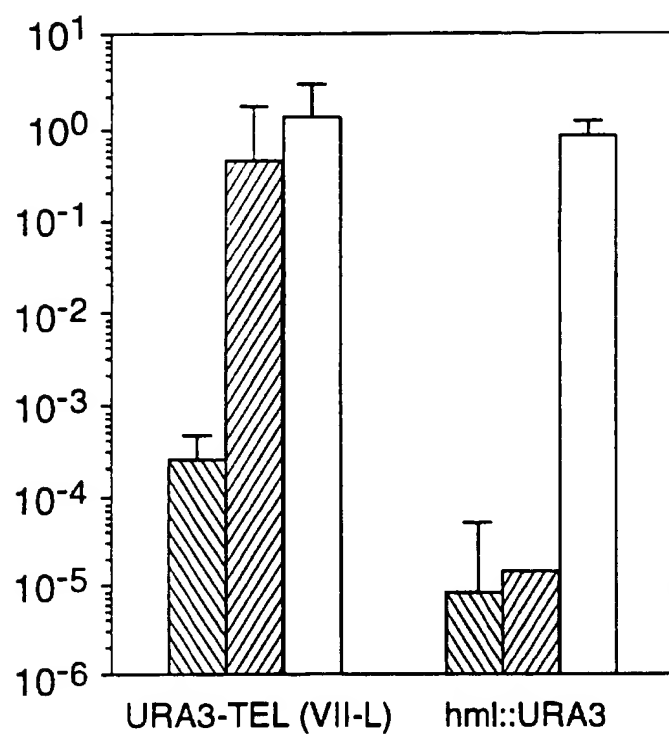


FIG. 1A

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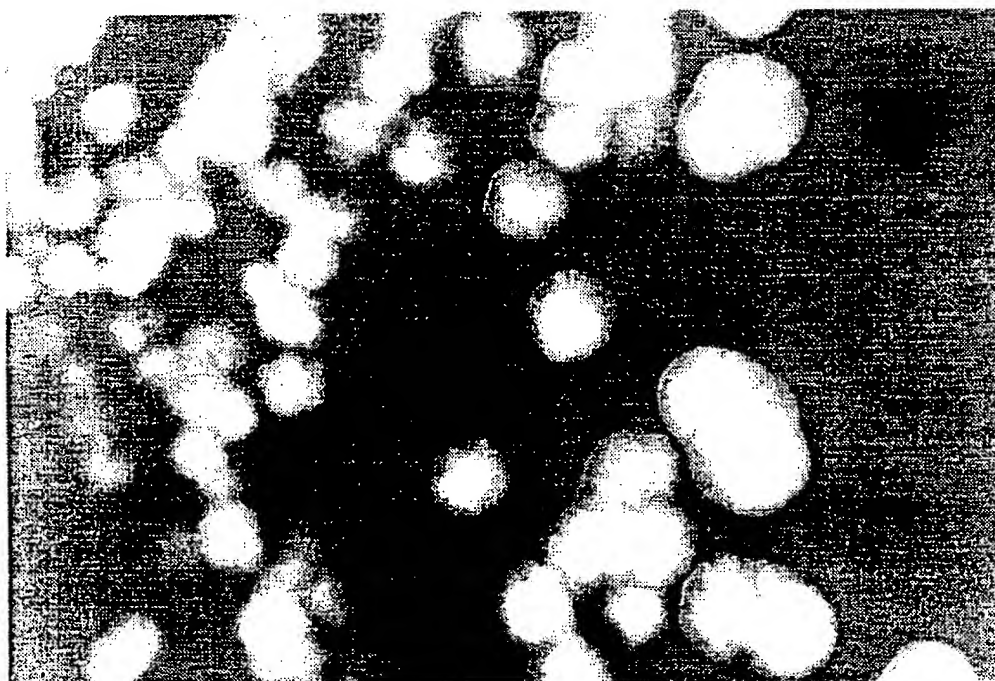


FIG. 1B

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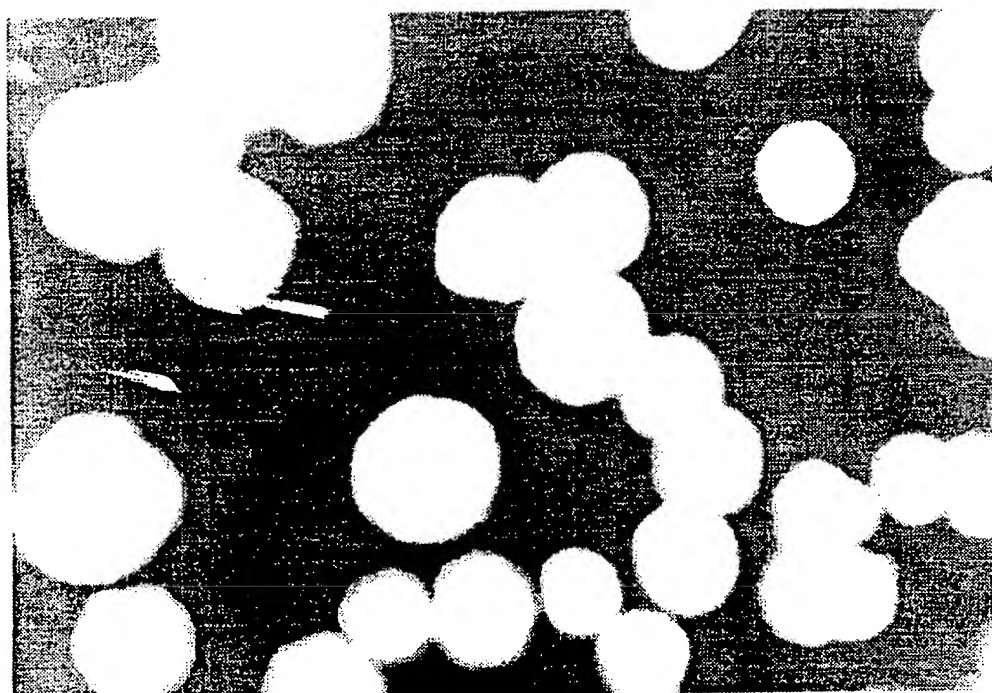


FIG.1C

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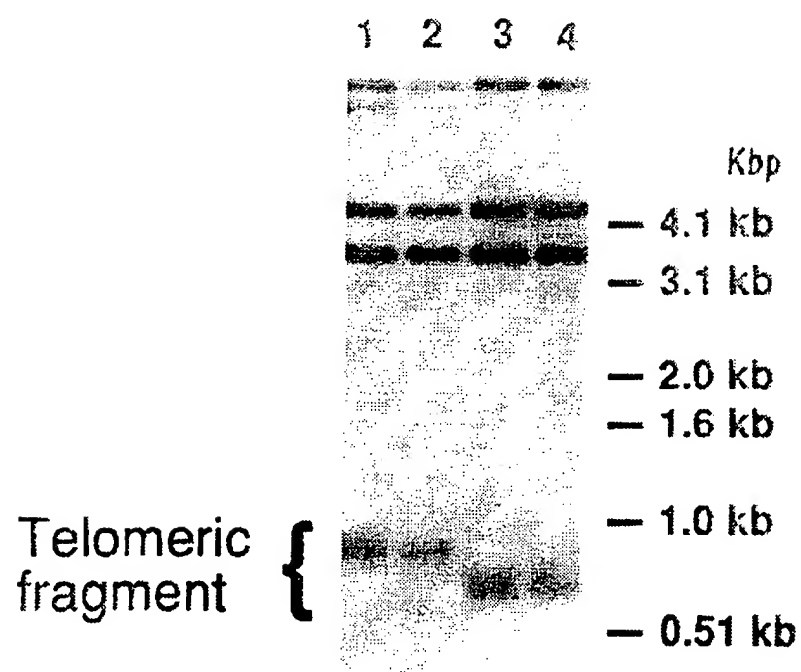


FIG.2

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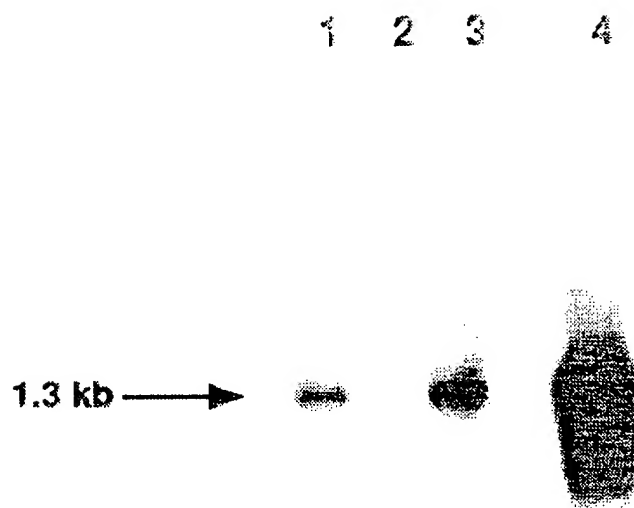


FIG.3A

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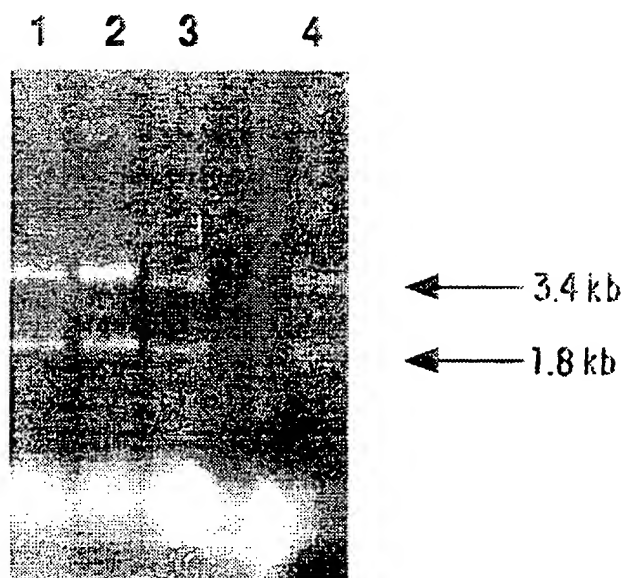
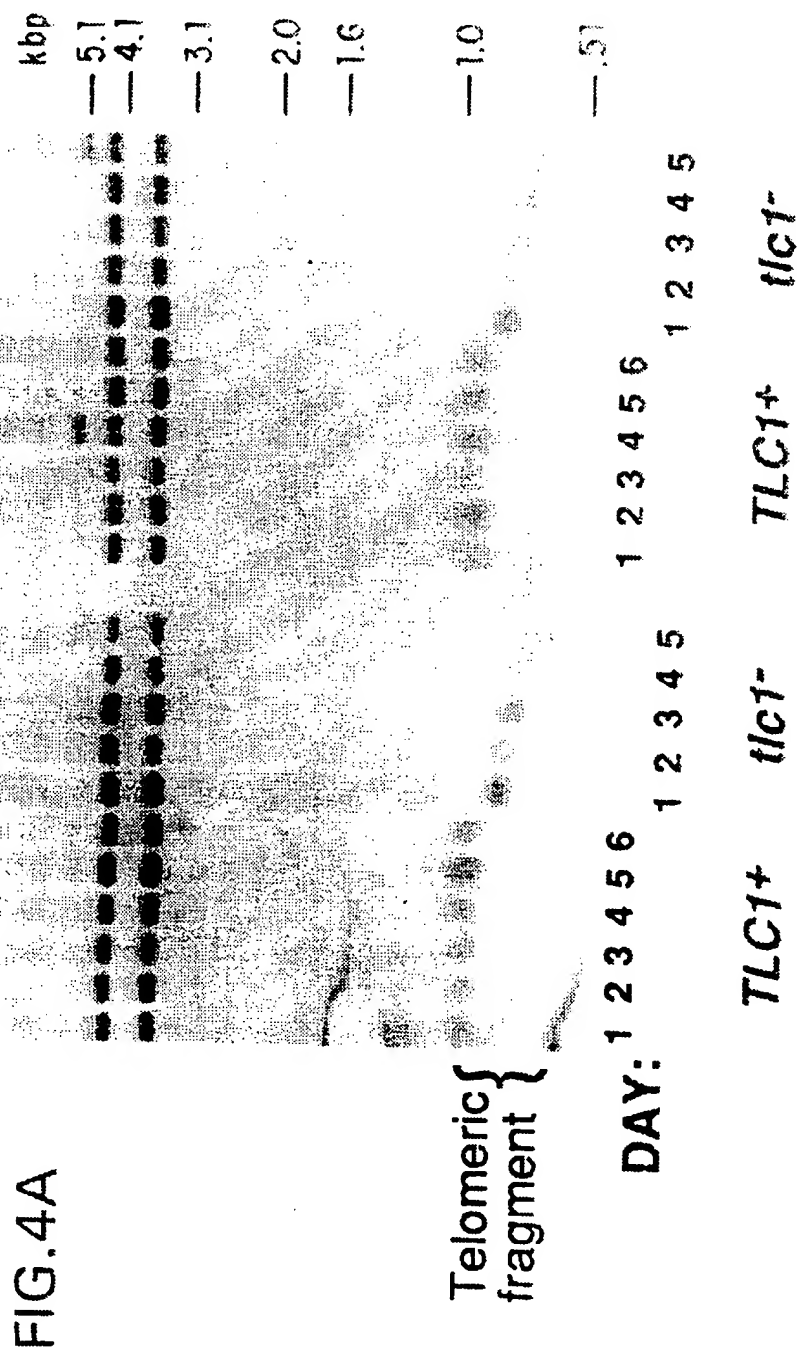


FIG.3B

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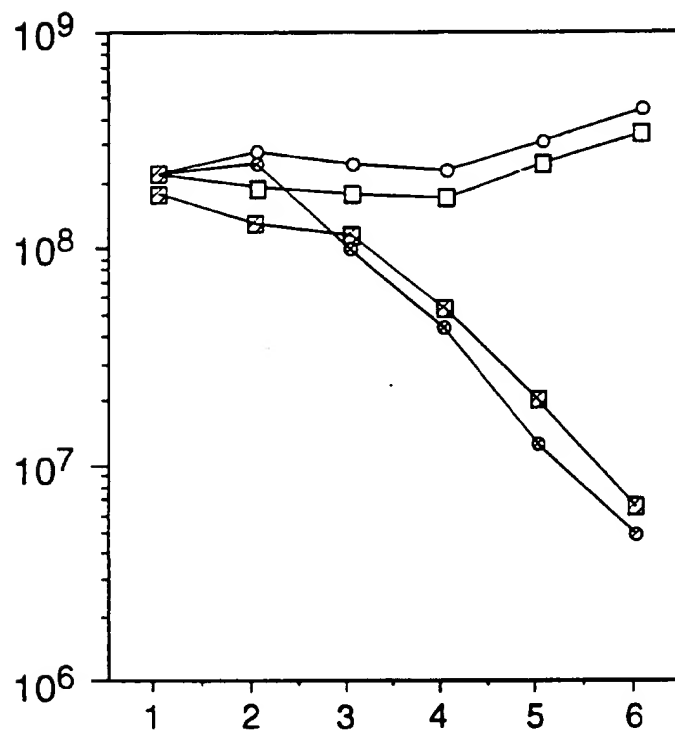


FIG. 4B

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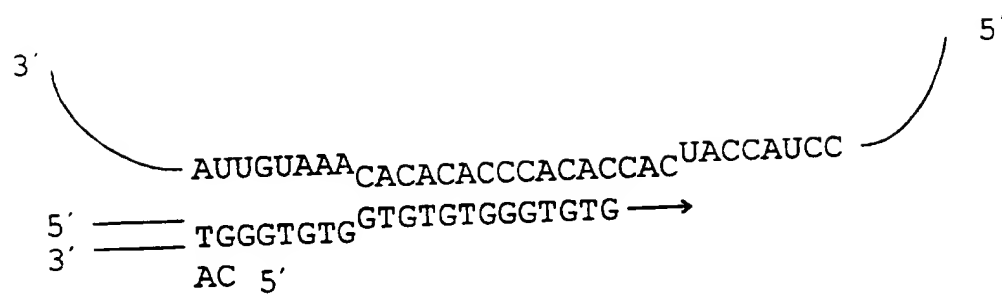


FIG. 5A

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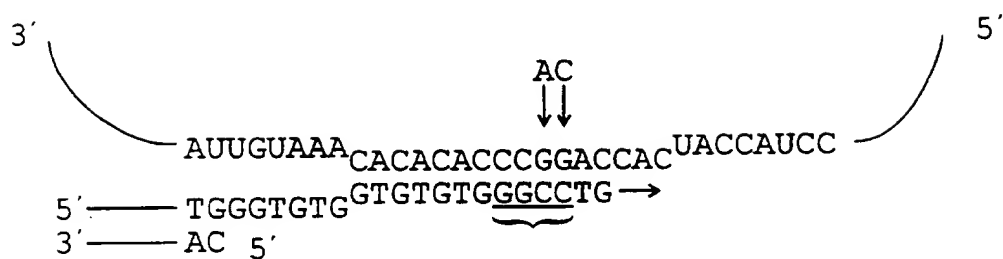


FIG. 5B

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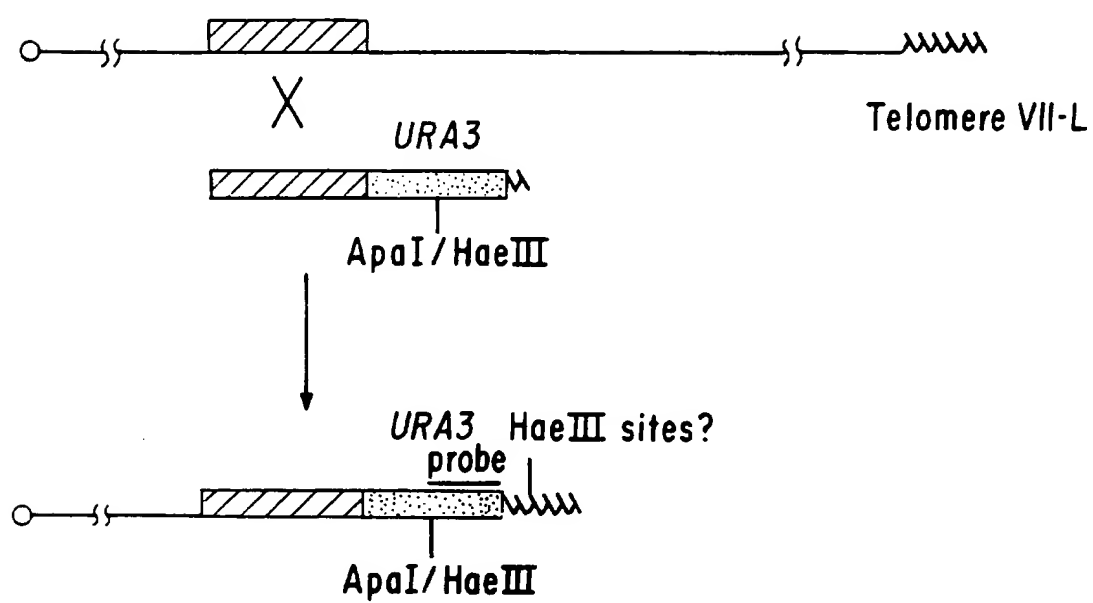


FIG. 6A

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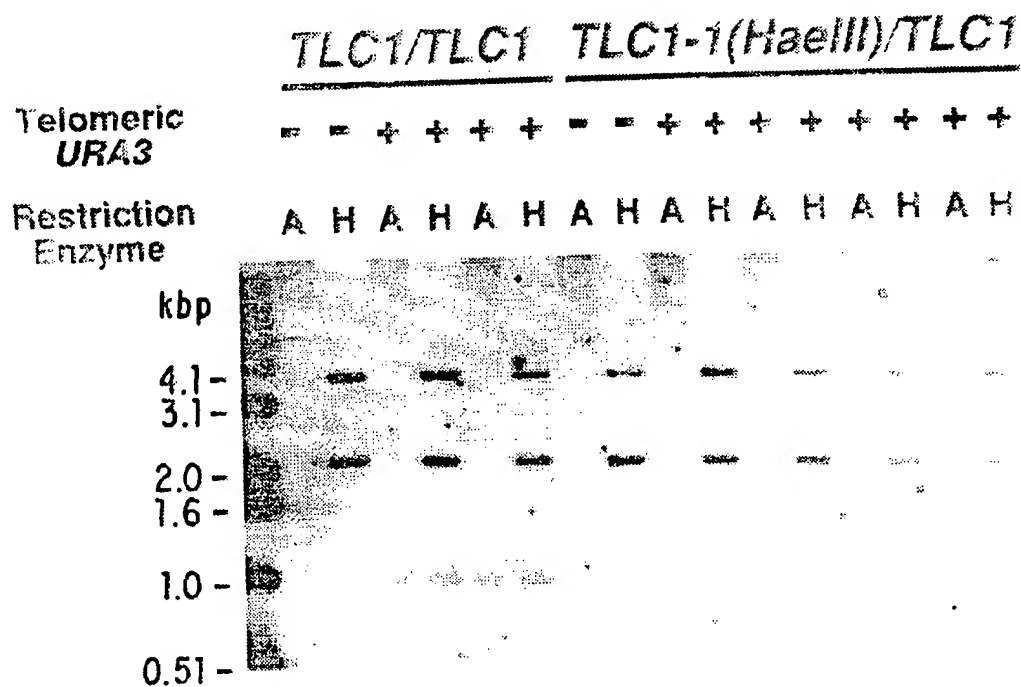
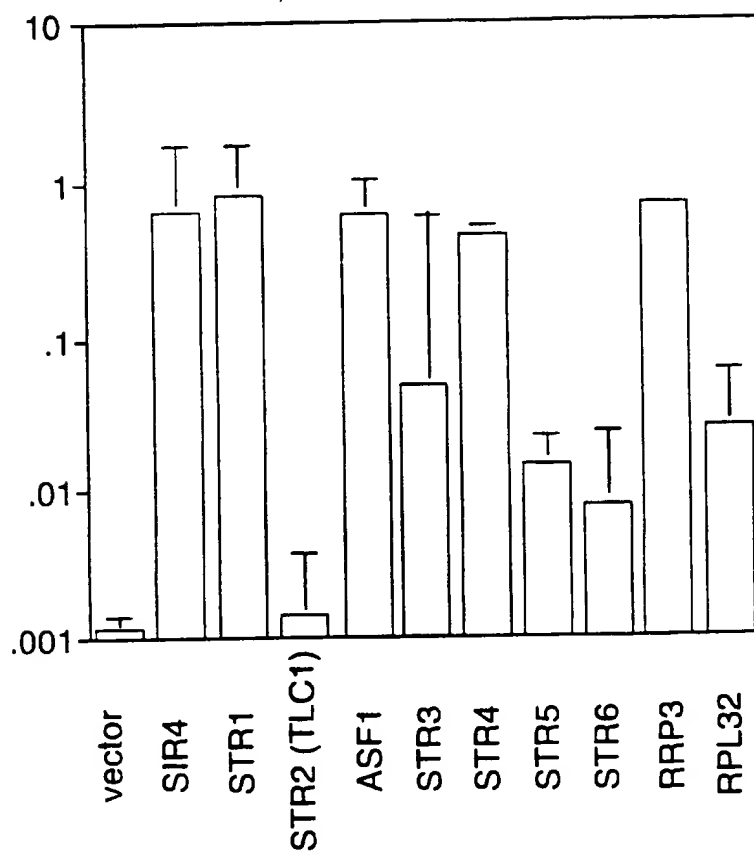


FIG.6B

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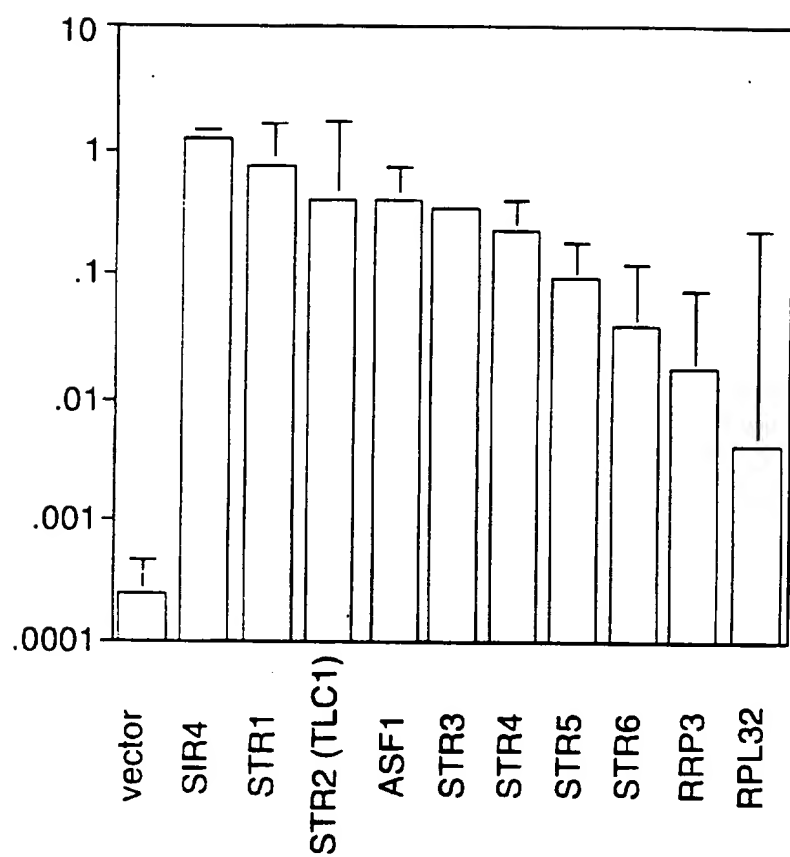


FIG. 7B

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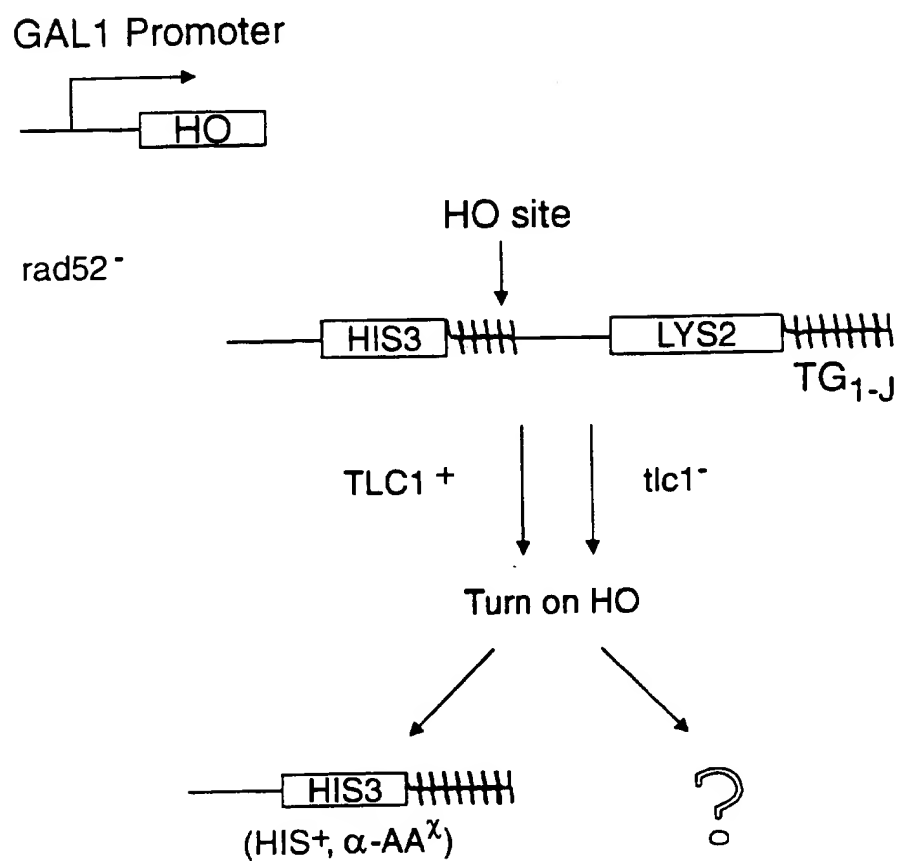


FIG. 8